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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:54:52; Search time 21 Seconds (without alignments)

27.477 Million cell updates/sec
Perfect score: 30
Sequence: 1 SVDVEX 6
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Searched: 283308 segs, 96168682 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

STY671 STY671 STY671 C;Species: Streptococcus pyogenes C;Apecies: Streptococcus pyogenes C;Becies: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 22-Jun-1999 C;Accession: 877671; 877672 R;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser Mol. Microbiol. 16, 509-519, 1995 A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococc A;Reference number: 877671; MUID:96037795; PMID:7565111 A;Accession: 877671 A;Residues: 1-128 «KAP> A;Cross-references: EMBL:U28853; NID:9818908; PIDN:AAA85729.1; PID:9818909 A;Residues: 1-128 «KAP> A;Cross-references: EMBL:U28853; NID:9818910; PIDN:AAA85729.1; PID:9818909 A;Residues: 1-128 «KAP> A;Accession: 877672 A;Accession: 877672 A;Accession: 577672 A;Accession: 1-128 «KAZ> A;Cross-references: EMBL:U28854; NID:9818910; PIDN:AAA85730.1; PID:9818911

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C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Accession: A00967
R;Jaccession: A00967
R;Jaccession: A00967
A;Title: Complete amino acid sequence of streptokinase and its homology with serine pro A;Reference number: A00967; MUID:83127125; PMID:6760891
A;Accession: A00967
A;Abolecule type: protein
A;Accession: A00967
A;Note: 169-Asp and 181-Asp were also found
A;Note: 169-Asp and 181-Asp were also found
A;Note: his protein is not a protease, but it activates plasminogen by complexing with C;Superfamily: streptokinase
C;Superfamily: streptokinase
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Cybace: Losept-1999 #Bequence_revision in-sep-1999 #Lear_commage_24-00-1999
R/Malke, H.; Roe, B.; Ferretti, J.J.
R/Malke, H.; Roe, B.; Ferretti, J.J.
A/Title: Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H
A/Reference number: A22801, MUD:85232082; PMID:2989113
A/Accession: A22801
A/Accession: A228
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C;Species: Streptcoccus sp.
C;Species: Ol-Dec-1989 #sequence_revision Ol-Dec-1989 #text_change 22-Jun-1999
C;Accession: S02723
R;Walter, F.; Siegel, M.; Malke, H.
Nucleic Acids Res, 17, 1852, 1989
A;Accession: S02723, MUID:89160265; PMID:2922269
A;Reference number: S02723; MUID:89160265; PMID:2922269
A;Mocession: S02723
A;Mocession: S02723
A;Mocession: S02723
A;Reference number: S02723; MUID:89160265; PMID:2922269
A;Reference number: S02723, MUID:89160265; PMID:2922269
A;Reference number: S02723, MUID:89160265; PMID:2922269
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C;Species: Streptococcus "equisimilis"
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
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C,Superfamily: streptokinase
                                                                                              208 SVDVEY 213
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Best Local Similarity
Matches 6; Conserv
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A13460
argenate reductase [imported] - Brucella melitensis (strain 16M)
C.Species: Brucella melitensis
C.Dete: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C.Datesion: A13460
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C.Datesion: A13460
R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, S.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Reference number: AD3252; PMID:11756689
A.Accession: A13460

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T05020
Cybbable lectin 2 precursor - alfalfa
CySpecies: Medicago sativa (alfalfa)
CySpecies: Medicago sativa (alfalfa)
CyBrecies: Medicago sativa (alfalfa)
CyBres: 16-Jul.1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
CyAccession: T09620
CyBrill, L.M.; Pieternel, V.R.
Submitted to the EMBL Data Library, March 1998
A,Bestription: Legume seed lectin genes: sequence of Mslec2 from Alfalfa, Alfalfa and SwA; Accession: T09620
A,Accession: T09620
A,Accession: T09620
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
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100.0%; Score 30; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels
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C;Keywords: calcium; glycoprotein; lectin
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-279/Product: probable lectin 2 #status predicted <MAT>
A,Experimental source: strain E2/M3
A,Note: allele 3
C,Genetics:
A,Gene: State
C,Superfamily: streptoxinase
C,Keywords: hydrolase; plasminogen activator; virulence
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A, Gene: lec2
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A;Cross-references: EMBL:Y16754
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A;Accession: T16011
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1207 <PAD>
A;Cross-references: EMBL:U00050; NID:9485108; PID:9485110; PIDN:AAA50695.1; CESP:F09F7...
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A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.; Lee
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R;Nolling, U; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AF01658; PIDN:AAB66044.1; GSPDB:GN00020; CESP:B0047.4
A;Experimental source: strain Bristol N2; clone B0047
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable phosphatase, HAD superfamily [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
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C'Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C'Accession: T16011
R;Pauley, A. the EMBL Data Library, May 1994
submitted to the EMBL Data Library, May 1994
A;Description: The sequence of C. elegans cosmid F09F7.
             hypothetical protein B0047.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                    R;Pauley, A.; Goela, D.; Ozersky, P. submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid B0047.
A;Reference number: 221102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F09F7.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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SIDVEY 30
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                           A; Residues: 1-186 <PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-215 < KUR>
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A, Status: preliminary
A, Molecule type: DNA
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79 SIDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP: B0047.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY
                                                                                                       C; Accession: T31951
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A; Introns: 51/2
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R;Walter, F.; Siegel, M.; Malke, H.
Nucleic Acids Res. 17, 1261, 1989
A;Title: Nucleotide sequence of the streptokinase gene from a Streptococcus pyogenes type A;Reference number: S02724; MUID:89160264; PMID:2646590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transferrin-like protein Ttf-1, salt-induced - green alga (Dunaliella salina)
C;Species: Dunaliella salina
C;Species: Tai012: Submited to University (1072)
R;Fisher, M.; Gokhman, I.; Pick, U.; Zamir, A.
Submited to the BMBL Data Library, November 1996
A;Reference number: 27101
A;Accession: T10729
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1274 <FIS>
A;Cross-references: EMBL:U77059; NID:g1684791; PID:g1684792
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: transferrin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptococcus pyogenes
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                      Gaps
A;Cross-references: EMBL:X13400; NID:g47095; PIDN:CAA31766.1; PID:g47096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-440 <WAL>
A;Cross-references: EMBL:X13399; NID:g47435; PIDN:CAA31765.1; PID:g47436
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptokinase A precursor - Streptococcus pyogenes (strain SF130/13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                 100.0%; Score 30; DB 2; Length 440; 100.0%; Pred. No. 28; 0; Indels cive 0; Mismatches 0; Indels
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                                                     A/Gene: skg
C;Superfamlly: streptokinase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-440/Product: streptokinase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Superfamily: streptokinase
F,1-26/Domain: signal sequence #status predicted <SIG>
F,27-440/Product: streptokinase #status predicted <MAT>
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100.0%; Pred. No. 90;
ive 0; Mismatches
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                         183 SVDVEY 188
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Matches 6; Conserv
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Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroerer, R.; Scoffone, F.; Sekfiguchi, J.; Sekowska, A.; Serol akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Toganoi, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpetra, P.; Tosato, V.; Uchlyama, A.; Authors: Yoshikawa, H.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gramapastive bacterium Bacillus subtilis. A; Accession: F69617
A; Accession: F69617
A; Mesediues: nucleic acid sequence not shown; translation not shown.
A; Meseidues: 1-311 < KUN
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-311 <XUN>
A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14858.1; PID:g2635363
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                major outer membrane protein - Fusobacterium nucleatum (strain FeVI) (fragment)
C;Species: Fusobacterium nucleatum
C;Species: Pusobacterium nucleatum
C;Species: O'Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60743 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60743 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60745 #seference number: A60745; MUID: 90257576; PMID: 2636259
A;Reference number: A60745
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: Drotein
A;Residues: 1-50 < BaXc>
A;Note: sequences of the homologous protein from strains F6, F3, and ATCC 10953 were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: X
A;Introns: 11/3; 63/1; 114/3; 166/2; 187/3; 233/3; 348/2; 405/1; 431/2; 473/1; 581/3
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ZC504.2 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 12-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C,Accession: T27619
R,Kershaw, J.
submitted to the EMBL Data Library, July 1995
A,Reference number: Z20394
A,Reference number: Z20394
A,Reference preliminary; translated from GB/EMBL/DDBJ
A,Geoule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-629 eWIL>
A,Cross-references: EMBL:Z50029; PIDN:CAA90341.1; GSPDB:GN00028; CESP:ZC504.2
A,Experimental source: clone ZC504
A,Gene: CESP:ZC504.2
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93.3%; Score 28; DB 2; Length 629;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
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C.Keywords: ATP; nucleotide binding; P-loop
F;168-175/Region: nucleotide-binding motif A (P-loop)
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58;
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Best Local Similarity
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SIDIEY 98
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Drimosome component (helicase loader) dnaI - Bacillus subtilis

C, Species accillus subtilis

C, Species Bacillus subtilis

C, Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 19-Jan-2001

C, Accession: B24720; C25680; F56017

R, Ogasawara, N.; Moriya, S.; Mazza, P.G.; Yoshikawa, H.

Nucleic Acids Res. 14, 9989-9999, 1986

A, Title: Nucleotide sequence and organization of dnaB gene and neighbouring genes on the A, Reference number: A93650; MUD:87117549; PMID:3027671

A, Residues: 1-311 < COAA

A, Residues: 1-314 < COAA

A, Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endo-1,4-beta-xylanase (EC 3.2.1.8) - Caldicellulosiruptor sp.
C.Species: Caldicellulosiruptor sp.
C.Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C.Accession: T31082
R.Morris, D.D.; Gibbs, M.D.; Ford, M.; Thomas, J.; Bergquist, P.L.
submitted to the EMBL Data Library, December 1997
A.Description: Family 10 and 11 xylanase genes from Caldicellulosiruptor sp. Rt69B.1.
A.Accession: T31082
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A;Molecule type: DNA
A;Residues: 1-11995 kMR>
A;Cross=references: EMBL:AF036923; NID:g2760904; FID:g2760908; PIDN:AAB95325.1
C;Genetics:
A;Gene: xynB
C;Keywords: glycosidase; hydrolase
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                                                                                                  A;Gene: CESP:F09F7.3
A;Introns: 23/1; 297/3; 600/2; 630/2; 724/3; 789/3; 916/1; 1102/2; 1150/3
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                           1; Mismatches
                              A; Experimental source: strain Bristol N2
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Cyfaces in B8542
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe Iller, L., Grotheck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
A;Ritle: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Residues: Draiminary
A;Molecule type: DNA
A;Residues: 1-271 <STO>
A;Residues: 1-271 <STO>
A;Residues: 1-271 <STO>
A;Residues: GB:AE005174; NID:g12516359; PIDN:AAG57198.1; GSPDB:GN00145; UWGP:23
A;Reperimental source: strain O157:H7, substrain EDL933
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C;Species: Pusobacterium nucleatum
C;Species: Pusobacterium nucleatum
C;Species: Pusobacterium nucleatum
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Nov-2000
C;Accession: 846435; 851507
R;Boletad, A.I.; Tommassen, J.; Jensen, H.B.
Mol. Gen. Genet. 244, 104-110, 1994
A;Title: Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nu A;Accession: 846435
A;Accession: 846435
A;Status: preliminary
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                    Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001
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83.3%; Pred. No. 1.2e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
86;
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Pred. No. 86;
1; Mismatches
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RPBOlstad, A.I.
submitted to the EMBL Data Library, August 1994
A;Reference number: S51507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Fusobacterium nucleatum
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83.3%;
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Best Local Similarity 83.3
Matches 5, Conservative
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Species: Escherichia coli
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Matches 5; Conserv
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59 SVDVQY 64
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S46435
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                                                                                                                                                                                                                                                                                                                                                                                                                        protein B0244.9 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88465
Exanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID: 99059613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Retsus: preliminary
A;Retsus: preliminary
A;Retsus: preliminary
A;Residues: 1-180 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 17
(990898
probable tail fiber protein [imported] - Escherichia coli (strain 0157:H7, substrain RIM c)Species: Escherichia coli
C)Species: Escherichia coli
C)Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C)Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
R)Haysshi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, R.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc A;Accession: G90898
A;Accession: G90898
A;Accession: G90898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <AXY
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BB5842
hypothetical protein Z3309 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:chr_III; PIDN:AAA68377.1; PID:9861357; GSPDB:GN00021; CESP:B0244
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics: EC82159
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                                                                 Length 50;
                                                                                                                                  0; Indels
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Pred. No. 86;
1; Mismatches
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                                                             Score 27; DB 2
Pred. No. 13;
1; Mismatches
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Pred. No. 55;
1; Mismatches
                                                                    90.08;
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Best Local Similarity 83.3%,
Asa 5; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
   C; Keywords: membrane protein
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SVDVQY 43
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SMDVEY
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A;Gene: B0244.9
A;Map position: 3
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accesion: E70598
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.
A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Protein Sequence Database, May 1996
A;Reference number: S65251
A;Accession: S65255
A;Molecule type: DNA
A;Residues: 1-391 «URW»
A;Cross-references: EMBL: Z73S86; NID:g1370475; PID:e246942; PID:g1370476; MIPS:YPL230w
A;Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-391 <RIE>
A;Residues: 1-391 <RIE>
A;Cross-references: BMBL:Z73586; NID:g1370475; PID:e246942; PID:g1370476; MIPS:YPL230w
A;Experimental source: strain S288C (AB972)
R;Urrestarazu, L.A.; Vissers, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispeciaes: Saccharomyces corevision 12-Apr-1996 #text_change 19-Apr-2002 Cispeciaes: Saccharomyces corevision 12-Apr-1996 #text_change 19-Apr-2002 Cispaces: Saccharomyces corevision 12-Apr-1996 #text_change 19-Apr-2002 Cisccession: S61704; S65249; S65255

Ribrestaratu, L.A. submitted to the EMBL Data Library, December 1995

A;Reference number: S61699

A;Reference number: S6169

A;Residues: 1-391 cura

A;Residues: 1-391 cura

A;Residues: BRBL:X94561; NID:g1181252; PID:e217970; PID:g1181258

Rightequer, M.; Mueller-Auer, S.; Schaefer, M.

Submitted to the Protein Sequence Database, May 1996

A;Reference number: S65202
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription factor YPL230w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein P1421
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genteltos:
A;Gene: £1382
C;Superfamily: phage lambda hypothetical protein 401
                                                                                                                                 90.0%; Score 27; DB 2; 183.3%; Pred. No. 1.2e+02; ive 1; Mismatches 0
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Pred, No. 1.3e+02;
1; Mismatches 0
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Similarity 83.3%;
5; Conservative
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                                                                                                                                                                                       5; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                         Local Similarity
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Social fonA precursor - Fusobacterium nucleatum (ATCC 10953)

NyAlternate names: major outer membrane protein, 40K

C;Species: Fusobacterium nucleatum
A;Variety: ATCC 10953

C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Oct-1999

C;Accession: 546436, 551508

Mol. Gen. Genet. 244, 104-110, 1994

A;Title: Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nucleatence number: $46435; MUD:94316187; PMID:8041356
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Submitted to the EMBL Data Library, March 1993

Ribolated, A.I.
Submitted to the EMBL Data Library, March 1993

Riference number: S51508

A;Reference number: S51508

A;Status: preliminary

A;Molecule : 179e: 104

A;Residues: 1-38, E', 40-338, 'G', 340-363, 'S', 365-371 <BOW>
A;Residues: EMBL:X72583; NID:g551439; PIDN:CAA51173.1; PID:g551440

A;Experimental source: ATCC 10953
                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156,'K',158-368 <BO2>
A;Cross-references: EMBL:X72582; NID:g530295; PIDN:CAA51172.1; PID:g530296
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                                                                                                                                                      90.0%; Score 27; DB 2; Length 368
83.3%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
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83.3%; Pred. No. 1.2e+02;
.ive 1; Mismatches 0; Indels
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-371/Product: porin #status predicted <MAT>
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Matches 5, Conservative
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A,Molecule type: DNA
A,Residues: 1-371. <BOL>
A,Cross-references: EMBL:X72583
                                                                                                                                                      Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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SVDVQY 64
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probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli (Species: Escherichia coli (CjDate: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 17-May-2002 C;Accession: E90968 R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Fitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: E90968 A;Accession
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C;Species: Escherichia coli
C;bete: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
C;Accession: H90854
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A;Molecule type: DNA
A;Residues: 1-47 < HAX>
A;Residues: 1-47 < HAX>
A;Crosa-references: GB:BA000007; PIDN:BAB36364.1; PID:g13362410; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                 Gaps
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C;Superfamily: phage lambda hypothetical protein 401
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C;Superfamily: phage lambda hypothetical protein 401
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                 5; Conservative
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SMDVEY 55
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G90907
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C.Species: Escherichia coli
C.Species: Bscherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C.Accession: G90907
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
G.Accession: G90907
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A.Accession: G90907
A.Accessio
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A.Accession: G43010
A.Molecule type: DNA
A.Residues: 1-401 < CAN>
R.Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
B.Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
A.Title: Nucleotide sequence of bacteriophage lambda DNA.
A.Reference number: A32891; MUD:83189071; PMID:6221115
A.Accession: B31016
A.Ac
A;Molecule type: DNA
A;Residues: 1-399 <COL>
A;Cross-references: GB:204121; GB:AL123456; NID:g3261736; PIDN:CAB08082.1; PID:e312285;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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hypothetical protein 401 - phage lambda

hypothetical protein 401 - phage lambda

N.Alternate names: orf-401; orf401

C.Species: phage lambda

C.Jacte: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999

C.Accession: G43010; D43016; A04389

R.Daniels, D.

Submitted to the Nucleic Acid Sequence Database, September 1982
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83.3%; Pred. No. 1.3e+02;
cive 1; Mismatches 0; Indels
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A.Gene: ECs2231
C.Superfamily: phage lambda hypothetical protein 401
C.Superfamily: phage lambda hypothetical protein 401
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Pred. No. 1.4e+02;
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Best Local Similarity 83.3
Matches 5; Conservative
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50 SMDVEY 55
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C; Superfamily: phage lambda hypothetical protein 401
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Best Local Similarity 83.34
...rhes 5; Conservative
                                                                                Query Match 90.0
Best Local Similarity 83.3
Matches 5, Conservative
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52 SMDVEY 57
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A85741
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C90769
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: C90769
R;Hayashi, T.; Maxino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasuunga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Tutle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Accession: C90769
A;Atterence number: A99629; MUID:21156211; PMID:11258796
A;Accession: C90769
A;Accession: C90769
A;Accession: C90769
A;Accession: C90769
A;Accession: C90769
A;Cross-references: GB:BA000007; PIDN:BAB34546.1; PID:g13360583; GSPDB:GN00154
A;Escherics:
C;Genetics:
A;Genetics:
A;Genetics:
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2011

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: H9084

A;Acutes preliminary

A;Molecule type: DNA

A;Residues: 1-437 c4Ax>

A;Residues: 1-437 c4Ax>

A;Cross-references: GB:BA000007; PIDN:BAB35231.1; PID:g13361273; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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Pred. No. 1.5e+02;
1; Mismatches 0;
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C;Superfamily: phage lambda hypothetical protein 401
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Best Local Similarity 83.3.
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50 SMDVEY 55
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Probable tail fiber protein of prophage CP-9330 Z2147 [imported] - Escherichia coli (St C; Species: Escherichia coli C; Species: Serba-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002 C; Accession: A85719

R; Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Gorobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, S29-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Accession: A85719

A; Status: preliminary
A; Accession: A85719
A; Status: preliminary
A; Residues: Lype: DNA
A; Residues: Lype: DNA
A; Residues: Lype: DNA
A; Residues: Lype: DNA
A; Cross-references: GB:AE005174; NID:g12515104; PIDN:AAG56213.1; GSPDB:GN00145; UWGP:Z2
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: Z2147
C; Superfamily: phage lambda hypothetical protein 401
                                                                                                                                                                                                                                                                                                                                                                                                                          probable tail fiber protein of prophage CP-933U 23074 [imported] - Escherichia coli (st. 5; Species: Bscherichia coli (5; Species: Bscherichia coli (5; Species: Bscherichia coli (5; Species: Bscherichia coli (5; Species: I6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002 (7, Accession: BsSsl. R.) Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001 A; Aritle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A88480; MUID:21074935; PMID:11206551
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A;Molecule type: DNA
A;Residues: 1-419 <STO>
A;Cross-references: GB:AE005174; NID:g12516091; PIDN:AAG56993.1; GSPDB:GN00145; UWGP:Z3
A;Experimental source: strain O157:H7, substrain EDL933
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83.3%; Pred. No. 1.5e+02;
iive 1; Mismatches 0; Indels
    Length 439;
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90.0%; Score 27; DB 2; 183.3%; Pred. No. 1.5e+02; iive 1; Mismatches 0
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C,Superfamily: phage lambda hypothetical protein 401
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A; Gene: F18B13.1
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Best Local S
Matches 5
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hypothetical protein Z2340 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: Dialentichia coli C;Date: Dialentichia coli (strain O157:H7, substrain EDL9 C;Accession: A85741

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A;Ritle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Rocession: A85741

A;Rocession: A85741

A;Status: preliminary
A;Rocession: A8574

A;Roce
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUDD:21074935; PMID:11206551
A;Residues: preliminary
A;Accession: F85584
A;Status: preliminary
A;Accession: F85584
A;Cross-references: GB:AE005174; NID:g12513753; PIDN:AAG55138.1; GSPDB:GN00145; UWGP:209
A;Cross-references: Strain O157:H7, substrain EDL933
C;Genetics: A;Gene: 20982
C;Superfamily: phage lambda hypothetical protein 401
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H181971
Probable ABC transporter ATP-binding protein NWA0535 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81971
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Accession: H81971
A;Accession: H81971
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-621 < PAR>
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53 SMDVEY
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ABC transporter, ATP-binding protein NMB1919 [imported] - Neisseria meningitidis (strai C;Species: Neisseria meningitidis
C;Species: Neisseria: N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Pleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamanhevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-621 aTET>
A;Experimental source: Serogroup B, strain MCS8
C;Genetics: Asseria and MCS8
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Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: O.Mara-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 (Spacesion: B56830 Mara-2001 (Spacesion: B56830 Mara-2001 (Spacesion: B56830 Mara-2001 (Spacesion: B56830 Mara-2001 Mara-2001 (Spacesion: B56830 Mara-2001 (Spacesion: B56830 Mara-2001 (Spacesion: B7, Mara-2001 Mara-20
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83829.1; PID:g73792 A;Experimental source: serogroup A, strain 22491 Cgenetian Cource: A;Genetian Cabs A;G
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C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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C, Superfamily: heat shock protein
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380 NVDVEY 385
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probable membrane protein of prophage CP-933X Z1918 [imported] - Escherichia coli (stra C;Species: Bscherichia coli (cjoate: 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: C8569; Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: C8569; Species: 11, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptidase related protein [imported] - Sulfolobus solfataricus
[Species: Sulfolobus solfataricus [Species: Sulfolobus solfataricus [Species: Sulfolobus solfataricus [Species: Sulfolobus solfataricus complete genome.]

Albestription: Sulfolobus solfataricus complete genome.

Albestription: Sulfolobus solfataricus complete genome.

Albestription: Sulfolobus solfataricus complete genome.

Albestription: Sulfolobus solfataricus complete genome.
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A;Residues: 1-973 <STO>
A;Cross-references: GB:AE005174; NID:g12514847; PIDN:AAG56007.1; GSPDB:GN00145; UMGP:Z1
Experimental source: strain O157:H7, substrain EDL933
A;Gene: Z1918
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C;Species: Escherichia coli
C;Species: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64897 #109189
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A,Residues: 1-1077 <KUR>
A,RCossar references: GB:AE006641; NID:g13815479; PIDN:AAK42355.1; GSPDB:GN00155
C;Genetics:
A,Gene: SSO2181
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A;Molecule type: DNA
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ilarity 83.3%; Pred. No. 3.6e+02;
Conservative 1; Mismatches 0;
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Pred. No. 4e+02;
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Similarity 83.3%;
5; Conservative
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52 SMDVEY 57
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Matches 5; Conserv
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R; Sugimoto, M.; Suzuki, Y.
J. Biochem. 119, 500-505, 1996
A; Title: Molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucosid A; Reference number: JC4624
A; Molecule type: MUD:96271012; PMID:8830045
A; Molecule type: MUD:96271012; PMID:8830045
A; Molecule type: DDBJ:D67034; NID:91498134; PIDN:BAA11053.1; PID:91498135
A; Molecule type: protein
A; Residues: 1-84 a SG143
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778 a SUG2>
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778
A; Note: the source is designated as Mucor javanicus IFO4770
C; Comment: This enzyme is an exo-carbohydrase, and catalyzes the splitting of an alpha-gwell as soluble starch.
C; Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog C; Reywords: glycoprotein; glycopidase; homology a SIM>F;187,364,406,466,500,568,734/Binding site: carbohydrate (Asn) (covalent) #status predicted
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B90835
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: B90835
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yanunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90835
A;Accession: B90835
A;Accession: Byoss A;Accession: Byoss A;Accession: Byoss A;Residues: 1-971 cHAY
A;Rolecule type: DNA
A;Residues: 1-971 cHAY
A;Residues: 1-971 cHAY
A;Residues: 1-971 cHAY
A;Esperimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Genetics:
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Pred. No. 3.6e+02;
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Query Match 90.0
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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75 TVDVEY 80
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Matches 5; Conserv
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Nototable and Voltes of Recent Procession of Page 2018 (1918)

Nototable 46x Potcable 58x Patchern) 68x Protein; cylindrical inclusion p (Species: papava ringspot virus, RNS process)

Obacca 50. Sep.1939 a Resquence revision 2.0.4Mg1994 #text_change 02-Feb-2001

CyAccession: J01899; P00509; A56609; S24785; S35725

Notession: J01899; P00509; A56609; S24785; S35725

Notession: J01899; P00509; A56609; S24785; S35725

Notession: J01899; MUD: 3101906; PMID: 1402799

Notession: J01899; MUD: 3101906; PMID: 145896

Notession: J01899; MUD: 31019009; PMID: 145896

Notession: J01899; MUD: 31019009; PMID: 145896

Notession: J01899; MUD: 31090099; PMID: 1458996

Notession: J01899; MUD: 31090099; PMID: 1458996

Notession: J01899; MUD: 310996

Notession: J01899; MUD: 31090099; PMID: 1458996

Notession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000007; PIDN:BAB35957.1; PID:g13362001; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h Similarity 83.3%; Score 27; DB 2; Length 3344; Similarity 83.3%; Pred. No. 1.4e+03; 5; Conservative 1; Mismatches 0; Indels
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22;
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Pred. No.
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149 SVDLEY 154
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A/Residues: 1-1471 cHAA>
A/Residues: 1-1471 child chi
A;Residues: 1-1122 <BLAT>
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636;
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636;
A;Experimental source: strain K-12, substrain MG1655
R;Aiba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Kasai, H.
.; Moromura, K.; Nakade, S.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; Saito, DNA Res. 3, 363-377, 1996
A;Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the A;Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the A;Title: A 570-kb DNA sequence of the GB/EMBL/DDBJ
A;Accession: T09189
A;Accession: T09189
A;Accession: Dreliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;References: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the yeast MY02
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NyAlternate names: protein YAL029c
NyAlternate names: protein YAL029c
NyAlternate names: protein YAL029c
C,Species: Saccharomyces cerevisiae
C,Species: Saccharomyces cerevisiae
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002
C,Accession: S30709, 551991
S4,Haarer, B.K.; Brown, S.S.
submitted to the EMBL Data Library, March 1992
A,Description: Identification of a yeast myosin gene that is similar to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 5.7e+02;
1; Mismatches 0; Indels
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Pred. No. 4.2e+02;
1; Mismatches 0; Indels
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83.38;
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Similarity 83.3%;
5; Conservative 1
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Best Local Similarity 83...
5, Conservative
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A;Accession: S30790
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SMDVEY 57
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero:
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF7727
A;Status: preliminary
A;Accession: Preliminary
A;Residues: 1-47 PAR>
A;Residues: 1-47 PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05520.1; PID:gl6503024; GSPDB:GN00176
C;Genetics:
A;Gene: STY1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiDate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
CiAccession: T08801
RiAnsorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
A;Reference number: 216472
A;Accession: T08801
A;Molecule type: mRNA
A;Residues: 1-93 <ANS>
A;Cross-references: EMBL:AL050196
C;Genetics:
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp586D2223.1 - human (fragment)
                                                                                                                                                                                                                                                                                                  86.7%; Score 26; DB 2;
100.0%; Pred. No. 22;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
73
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Pred. No. 46;
1; Mismatches
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S; Conservative
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nes 5; Conserv
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20 SVEVEY
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Matches 5
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Job time
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CiDate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change Ol-Mar-2002

CiDate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change Ol-Mar-2002

CiAccession: #64943

Ralattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Reference number: A64720; MUID:97426617; PMID:9278503
A.; Reference number: A64720; MUID:97426617; PMID:9278503
A.; Reference number: A64720; MUID:97426617; PMID:9278503
A.; Restauts: nucleic acid sequence not shown; translation not shown
A.; Molecule type: DNA
A.; Residence: 17-7 ** CBLAT>
A.; Residence: 17-7 ** CBLAT>
A.; Residence: Strain K-12, substrain MG1655
                                                                                                                                                                                                                                             C.Species: Escherichia coli
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C.Species: N.T.; Plunket III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
ArTitle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A.Reference number: A88480; MUID:21074935; PMID:11206551
A.Accession: A85794
A.Accession: Preliminary
A.Residues: 1-47 <STO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005174; NID:g12515870; PIDN:AAG56813.1; GSPDB:GN00145; UMGP:Z28
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                  RESULT 47
A85794
hypothetical protein 22869 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
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AF0727

conserved hypothetical protein STY1968 [imported] - Salmonella enterica subsp. enterica conserved hypothetical protein STY1968 enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0727

R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Main, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gaora, P.
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Q89023 mus musculu
Q9244 mucor javan
P76072 escherichia
P7610 pgenome po
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P7611 paemophilus
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P76373 escherichia
P76413 percoccus
Q94910 escopyrum p
Q4457 agrobacteri
P2982 myxoma viru
P6983 myxobacteri
P02680 rattus norv
O65932 mycobacteri
Q89wyb3 thermoccus
Q8wyb3 thermocia
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25.651 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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P10520;
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                            serine proteases.";
Biochemistry 21:6620-6625(1982).
-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES
-!- PLASMINOGEN BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malke H., Roe B., Ferretti J.J.;
"Nucleotide sequence of the streptokinase gene from Streptococcus
equilabilis H46A.";
Gene 34:357-362[1985].
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SACCHARIDE-BINDING AND CELL-AGGLUTINATING ACTIVITIES. SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
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MEDLINE=85232082; PubMed=2989113;
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MEDLINE=83127125; PubMed=6760891;
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01-APR-1988 (Rel. 07, Last sequ
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                             EMBL; X60387; CAA42938.1; -. HSSP; P04122; 1LOE.
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Matches 6; Conservative
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NCBI_TaxID=119602;
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IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE INVASIVENESS OF THE CELLS.
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-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES
PLASMINGERS BY COMPLEXING WITH IT. AS POTEWRIAL, VIRULENCE FACTOR,
IT IS THOUGHT TO PREVENT THE FORMATION OF BFFECTIVE FIBRIN
BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE
INVASIVENESS OF THE CELLS.
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STRAIN=SF370 / ATCC 700294 / Serotype M1;

STRAIN=SF31192684; PubMed=11296296;

MEDLINE=21192684; PubMed=11296296;

MEDLINE=21192684; PubMed=11296296;

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar P.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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STRAIN=SF130/13 / Serctype M1;
MEDLINE=89160264; PubMed=2646590;
MEDLINE=9160264; PubMed=2646590;
MEDLINE=7, Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene from a Streptococcus
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                                                                                                                                                                                                                                                                                 EMBL; K02986; AAA26974.1; -.
EMBL; X72832; CAA51351.1; -.
PIR; AA2801; AA281.1; -.
PDR; 1QQR; 03-MAY-00.
InterPro; IPR004093; Staphylokinase.
PF02821; Staphylokinase; 3D-structure.
Plasminogen activation; Signal; Virulence; 3D-structure.
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8FC1F22648ACC77A CRC64;
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D -> L.
EXY -> LEYK (IN REF. 2).
N -> D (IN REF. 2).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Streptokinase A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pyogenes type I strain.";
Nucleic Acids Res. 17:1261-1261(1989).
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Gaps

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Length 440;

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100.0%; Score 30; 100.0%; Pred. No.

STREPTOKINASE G. 5521F8825FE1B6EA CRC64;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptcoccous.";

Nucleic Acids Res. 17:1262-1262(1989).

-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES

ELSMINGEN BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR,

IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN

BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE

INVASIVENESS OF THE CELLS.
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EMBL; AE006620; AAK34665.1; -.
PIR; S02724; S02724.
FICTPRO: IPROBA93; Staphylokinase.
Pfam; PF02821; Staphylokinase; 3.
Plasminogen activation; Signal; Virulence; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDINE = 2922269; MADINE = 8160265; PubMed = 2922269; MADINE = 816265; Siegel M., Malke H.; Maler F., Siegel M., Malke H.; Mucleotide sequence of the streptokinase gene from a group-G
                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 1; Length 440; 100.0%; Pred. No. 13; cive 0; Mismatches 0; Indels
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R -> G (IN REF. 1).
D -> N (IN REF. 1).
D -> X (IN REF. 1).
K -> N (IN REF. 1).
K -> N (IN REF. 1).
W, D6227EF040B758DB CRC64;
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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae,
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01-JUL-1989 (Rel. 11, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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InterPro; IPR004093; Staphylokinase.
Fam; PF02821; Staphylokinase; 3.
Plasminogen activation; Signal; Virulence.
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Thes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                             440
163
345
373
428
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163
345
345
373
428
438
440 AA;
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ID STRP_STRSP
AC P10519;
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CONFLICT
CONFLICT
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8686803, Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Pererson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hust M.A., Kaine B.P., Bordovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 9.1;
1; Mismatches 0; Indels
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ID DOUP WIGHER

CONTROL

OSCUTE:

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR 15-SEP-2003 (Rel. 42, Last annotation update)

OT 15-SEP-2003 (Rel. 42, Last annotation update)

Migglesworthia glossinidia brevipalpis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Complete proteome.
SEQUENCE 183 AA; 21756 MW; 769FCF680E86C895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0347.1.
                                                                                                                                                                                                                                         183 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
                                                                                                                                                                                                                                         STANDARD;
                                                   183 SVDVEY 188
1 SVDVEY 6
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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                         CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
                                                 SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
                                                                                                                                                                              SUBCELLULAR LOCATION: CYtoplasmic (Probable).
SIMILARITY: BELONGS TO THE UROPORPHYRINGGEN DECARBOXYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                            "Genome sequence of the endocellular obligate symbiont of tsetse files, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002)
                                                                                                                                                                                                                                                                                                                                     idamap; MF_00218; -; 1.
InterPro; IPR006361; HemE.
InterPro; IPR006361; HemE.
InterPro; IPR000257; Uro_decarbxyls.
ProDom; PD003225; Uro_decarbxyls; 1.
ProDom; PD003225; Uro_decarbxyls; 1.
TIGRPAMs; TIGR01464; hemE; 1.
PROSITE; PS00906; UROD_1; PALSE_NEG.
PROSITE; PS00907; UROD_2; 1.
Lyase; Decarboxylase; Porphyrin biosynthesis; Complete proteome. SEQUENCE 360 AA; 41359 MW; CA18CB13C1B8492B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.7%; Score 29; DB 1; Length 360; 83.3%; Pred. No. 19; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VAD6; Q8S2V9; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 15-SBP-2003 (Rel. 42, Last annotation update) Putative conserved oligomeric Golgi complex component 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              742 AA
                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                  PATHWAY: Porphyrin biosynthesis.
              Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                          EMBL; AB063522; BAC24654.1; -.
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Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 SVDIEY 277
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                         NCBI_TaxID=36870;
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RESULT 9
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lapidus A., Galleron N., Sorokin A., Ehrlich S.D., "Sequencing and functional annotation of the Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
MEDLINE=87117549; PubMed=3027671;
Ogasawara N., Morryya S., Mazza P.G., Yoshikawa H.;
"Nucleotide sequence and organization of dnaB gene and neighbouring genes on the Bacillus subtilis chromosome.";
Nucleic Acids Res. 14:9989-9999(1986).
            Hypothetical protein; Transport; Protein transport; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Bacillus
                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJNE=97124191; PubMed=8969504; Mipaths: Piper K., Mipaths., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J., Emmerson P.T., Harwood C.R.; The dnaB-pheA (256 degrees-240 degrees) region of the Bacil subtilis chromosome containing genes responsible for stress metabolism.;
                                                                   Length 742;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                       742 AA; 84075 MW; 85998EF365194E39 CRC64;
                                                                                            ;
0
                                                                Match 96.7%; Score 29; DB 1; Local Similarity 83.3%; Pred. No. 41; es 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
08-EFB-2003 (Rel. 41, Last annotation update)
Primosomal protein dnal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the 200 kb rrnB-dnaB region."; Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology 142:3067-3078(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98048467; PubMed=9387221;
PRINTS; PR00747; GLYHDRLASE47.
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                               682 SVDIEY 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
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P06567;
                         Membrane.
SEQUENCE
                                                                 Query Match
                                                                                          Matches
 SKKB
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Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schlecter R., Schroeter R., Scéffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Toseuchi M., Vandenbol M., Vannier F., Vossarotti A., Vistikama S., Vandenbol M., Vannier F., Vossarotti A., Vistikama S., Vamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87118226; PubMed=3027697;
Hoshino T., McKenzie T., Schmidt S., Tanaka T., Sueoka N.;
"Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for
DNA replication initiation and membrane attachment.";
Proc. Natl. Acad. Sci. U.S.A. 84:653-657(1987).
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Nucleic Acids Res. 20:1143-1143(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95291463; PubMed=7773414;
Bruand C., Ehrlich S.D.;
"The Bacillus subtilis dnaI gene is part of the dnaB operon.";
Microbiology 141:1199-1200(1995).
-!- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION.
-! SIMILARITY: SOME, TO DNAA FROM VARIOUS BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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        Primosome, DNA replication, ATP-binding, Complete proteome.

        NP BIND
        168
        175
        ATP (PROBABLE)

        CONFLICT
        19
        19
        K -> N (IN REF. 5).

        CONFLICT
        24
        24
        M -> T (IN REF. 5).

        SEQUENCE
        311 AA, 36114 MW, A86FC94AB6841264 CRC64;

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66.7%; Pred. No. 28;
iive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 AA
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EMBL; 299118; CAB14858.1; -...
EMBL; M15183; AAA22405.1; -...
PIR; B24720; IQBS44.
Subtinist; B010359; anal.
InterPro; IPR003593; AAA_ATPase.
SMART; SM00382; AAA; 1...
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1D TPP1 MOUSE STANDARD;
AC 089023; Q9QUS7;
DT 15-DEC-1998 (Rel. 37, Created)
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EMBL; Z75208; CAA99605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-206 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
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es 4; Conserv
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Serine protease; Zymogen; Signal; Lysosome;

EMBL; AJ011912; CAA09863.1; ALT_INIT. EMBL; AF124599; AAD32573.1; -. EMBL; AF111172; AAD03083.1; -.

EMBL; AK002418; BAB22085.1; -. MEROPS; S53.003; -.

MEROPS; S53.003; -. MGD; MGI:1336194; Cln2. Hydrolase; Protease; Se

Glycoprotein. SIGNAL PROPEP 2

CHAIN

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ESUGRENCE FROM N.A. SUBJECT STATES ST
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-!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity).

-!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a polypeptide, but also endopeptidase activity.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99142696; PubMed=9989590;
Vines D.J., Warburton M.J.;
"Classical late infantile neuronal ceroid lipofuscinosis fibroblasts are deficient in lysosomal tripeptidyl peptidase I.";
FEBS Lett. 443:131-135(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Sleat D.; Sleat D.E., Lobel P.; Lobel P.; "Murine homologue of the lysosomal pepstatin insensitive protesse which is deficient in human classical late infantile neuronal ceroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20028316; PubMed=10556422;
Katz M.L., Julu P.-C., Grob-Nunn S.E., Shibuya H., Johnson G.S.;
"Characterization and chromosomal mapping of a mouse ortholog of the
late-infantile ceroid-lipofuscinosis gene CLN2.";
16-OCT-2001 (Rel. 40, Last sequence update)
28-EEB-2003 (Rel. 41, Last annotation update)
Tripeptidyl-peptidase I precureor (EC 34.14.9) (TPP-I) (Tripeptidyl
aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Activated by autocatalytic proteolytical processing upon acidification (By Bimilarity).
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mamm. Genome 10:1050-1053(1999).
                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity).

-!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl
aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC).
CLN2 OR TPP1.
                                                                                                                                                   BY SIMILARITY.

REMOVED IN MATURE FORM (BY SIMILARITY)
TRIPEPTIDYL-PEPTIDASE I.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Activated by autocatalytic proteolytical processing upon acidification (By similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S53.
                                                                                                                                                                                                                   NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 1; Length 562; Pred. No. 91; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 OAF8163EA1A66396 CRC64;
                                                                                                                                                                                                                                                                                                                                             M -> V (IN REF. 1).
P -> LDPFVP (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                 61342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                   1
562 !
562 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 setter dogs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
TPP1_CANFA
ID TPP1_CANFA
AC Q9XSB8;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53

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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Side tail fiber protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION AS STF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruse
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                      274 SLDVEY 279
                                                                                                                                                                                                                                 389
563 AA;
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=10710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteriophages."
                                                                                                                                                                                                                                                                                                                1 SVDVEY
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Matches
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                                                                REMOVED IN MATURE FORM (BY SIMILARITY).
TRIPETIDYL-PEPTIDASE I.
BY SIMILARITY.
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blochim. Blophys. Acta 1384:233-242(1998).

-!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus. Maximum activity at pH 4, unstable above pH 7.

-!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive procease) (LPIC).
CLN2 OR TPP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Du P., Kato S., Li Y., Maeda T., Yamane T., Yamamoto S., Fujiwara M. Yamamoto Y., Nishi K., Ohkubo I., "Rat tripeptidyl peptidase I: its purification and molecular cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vines D.J., Warburton M.J.; "Purification and characterisation of a tripeptidyl aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
SUBCELLULAR LOCATION: Lysosomal.
PTM: Activated by autocatalytic proteolytical processing upon accidification (By similarity).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.
                     MEROPS; SS3.003; -.
Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome;
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 196-217; 374-392 AND 395-429, AND CHARACTERIZATION
                                                                                                                                                                                                  Score 27; DB 1; Length 563;
Pred. No. 91;
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                  21465A44C34934F4 CRC64;
                                                                                                                                                                                                                                                                                                                                     563 AA.
                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98323562; PubMed=9659384;
           EMBL; AF114167; AAD25043.1; -.
                                                                                                                                                                                  61362 MW;
                                                                                                                                                                                                     90.0%;
                                                                                                                                                                                                                     Similarity 83.3
5, Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                         195
195
563
360
475
517
                                                                                                                         210
222
286
313
                                                                                                                                                                      443
563 AA;
                                                                                                                                                                                                                                                                            274 SLDVEY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from rat spleen.";
                                                                                                                                                                                                                                                      1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                  20
360
360
360
475
517
210
222
286
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                                               Glycoprotein.
SIGNAL
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                                                                 ROPEP
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Hendrix R.W., Duda R.L.,
Hendrix R.W., Duda R.L.,
Hendrix R.W., Duda R.L.,
Hendrix R.W., Duda R.L.,
Handa Papa: not the mother of all lambda phages.",
Science 258:1145-1146 (1992).
-I- MISCELLANEOUS: The common laboratory strain of bacteriophage
lambda; lambda Papa; carries a frameshift mutation relative to Ur-
lambda, the original isolate. The Ur-lambda virions have thin,
jointed tall fibers (side tail fibers) that are absent from lambda
wild type. Relative to lambda PaPa, Ur-lambda has expanded
receptor specificity and adsorbs to E. coll cells more rapidly.
-!- SIMILARITY: BELONGS TO THE TAIL FIBER PAMILY.
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92165720; PubMed=1531648; Haggard-Liungquist E., Halling C., Calendar R.; Mungquist E., Halling C., Calendar R.; Macquences of the tail fiber genes of bacteriophage P2: evidence for horizontal transfer of tail fiber genes among unrelated
                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

NUCLEOPHILE (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-A (IN REF. 2).

VG -> SQ (IN REF. 2).

GGT -> SPP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                              EMBL; AB043870; BAB18570.1; -.
Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome;
Glycoprotein.
SIGNAL 1 19 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 1; Length 563; Pred. No. 91;
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HT -> SPP (IN REF. 2).

B54F3C86205DFEC1 CRC64;
                                                                                                                                                                                                                   BY SIMILARITY.
REMOVED IN MATURE FORM.
TRIPEPTIDYL-PEPTIDASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83189071; PubMed=6221115; Sanger F., Coulson A.R., Hong G.F., Hill D.F., Pete Sanger F., Coulson A.R., Hong G.F., Hill D.F., Pete "Nucleotide sequence of bacteriophage lambda DNA."; J. Mol. Bool. 162:729-773 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
modified and this statement is not removentities requires a license agreement (Soor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 174:1462-1477(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61332 MW;
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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or send an email.

NR EMBL; D67034; BAA11053.1; -.

DR PRO1052; Glyco_hydro_31.

DR PRO51TE; P800129; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.

FROSITE; P800707; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.

KW HYdrolase; Glycoprofein; Signal.

FT SIGNAL 23 864 ALPHA-GLUCOSIDASE.

STAN 30 BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).
  CORRECTED IN POSITION TO 396 TO RECREATE THE ORIGINAL STF PRIOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugimoto M., Suzuki Y.;
"Molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucosidase from Mucor javanicus.";
J. Blochem. 119:500-505(1996).
-I. FUNCTION: Hydrolyzes not only malto-oligosaccharides but also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   soluble starch.
-!- CATALYTIC ACTIVITY: Hydrolygis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           774 AA; 77527 MW; CDD1DF85E919123B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 27; DB 1; L
83.3%; Pred. No. 1.3e+02;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                      EMBL; J02459; AAA96555.1; ALT FRAME.
EMBL; J02459; AAA96557.1; ALT_FRAME.
PIR; C43009; QXBP2L.
InterPro; IPRO05003; Phage_fiber.
InterPro; IPR005068; Phage_fiber_2.
Pfam; PF03435; Phage_fiber; 6.
Pfam; PF03466; Phage_fiber; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96271012; PubMed=8830045;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.33,
Conservative 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||||
50 SMDVEY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=51122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-IFO 4570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucor javanicus.
                                                                                                                                                                                                                                                                                                                                                                                      Fiber protein.
SEQUENCE 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
AGLU MUCJA
1D AGLU MUCJA
DT 01-NOV-1997 (
DT 01-NOV-1997 (
DT 01-NOV-1997 (
DT 01-NOV-1997 (
DE Alpha-glucos)
OS MUCOC Javanic
OC MUCOC MOCO JAVANIC
OC MUCOC MOCO JAVANIC
OC Java
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Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Dana sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.",
DNA Res 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIB-KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
N-LINKED (GLCNAC. .) (POTENTIAL).
M-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90774; BAA14956.1; ...
EMBL; D90775; BAA14976.1; ...
ENGL; D90775; BAA14976.1; ...
ECGGENE, EG13370; BAG.
InterPro; IPR005003; Phage_fiber.
InterPro; IPR005068; Phage_fiber.
Pfam; PF03195; Phage_fiber.2;
Pfam; PF031406; Phage_fiber.2; ...
Hypothetical protein; Fiber protein; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                     ô
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STRANDARD; PRT; 1120 AA.

AC P76072; P77560;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Side tail fiber protein homolog from lambdoid prophage Rac.
GN STFR OR B1372.
                                                                                                                                                                                                                                                Score 27; DB 1; Length 864;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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      364 N-406 N-466 N-560 N-568 N-734 N-98761 MW;
                                                                                                                                                                                                                                                      90.08;
                                                                                                                                                                                                                                                                                  83.3%;
                                                                                                                                                                                                                                                                                                                     5; Conservative
         364
406
466
500
500
734
734
734
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gregor J., Davis
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
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CARBOHYD
                                                                                              CARBOHYD
                                                                                                                                                                                          SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE=92249563; Pubhed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
Storms R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=94334370; PubMed=8056830;
Marer B.K., Petzold A., Lillie S.H., Brown S.S.;
"Identification of MY04, a second class V myosin gene in yeast.";
J. Cell Sci. 107:1055-1064(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces
                                                                               ;
                                     Score 27; DB 1; Length 1120;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleotide sequence of chromosome I from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M90057; AAC37409.1; -.
EMBL; U12980; AAC05603.1; -.
PIR; S30790; S30790.
HSSP; P10587; 1BR2.
SGD; S000027; MY04.
GO; GO:000143; C:actin cap (sensu Saccharomyces); IDA.
InterPro; IPR00048; IQ. region.
InterPro; IPR00048; IQ. region.
InterPro; IPR006048; IQ. region.
InterPro; IPR0060409; Myosin_head.
InterPro; IPR01609; Myosin_head.
PF01643; DIL; 1.
113779 MW; 542E59D71EE795B4 CRC64;
                                                                                                                                                                                                                                                                                                       (Rel. 27, Created)
(Rel. 27, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                 1471 AA
                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00063; myosin head; 1.
Pfam; PF02736; Myosin N; 1.
PRINTS; PR0193; MYOSINHEAVY.
PRODOM; PD000355; myosin head; 1.
SMART; SM00015; IQ; 2.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                    Myosin-4 isoform.
MYO4 OR SHEI OR YAL029C OR FUN22.
                                       90.0%;
                                                                                 5; Conservative
                                                                                                                                                                                                                                                               STANDARD:
  1120 AA;
                                                                                                                                              |:||||
SMDVEY 55
                                                              Best Local Similarity
                                                                                                                       1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                         01-OCT-1993
                                                                                                                                                                                                                                                               MYS4 YEAST
P32492;
                                                                                                                                                                                                                                                                                                                          01-OCT-1993
15-SEP-2003
                                                                                                                                                               20
  SEQUENCE
                                         Query Match
                                                                                 Matches
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MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MAMAIG C.H., Yeb S.D.;

MILG, and non-papaya infecting strains of papaya ringspot virus.";

Arch. Virol. 127:345-354(1992).

LACH. Virol. 127:345-354(1992).

TRANSHISSION AND ALSO HAS PROTEINHAE IS REQUIRED FOR APHID

TRANSHISSION AND ALSO HAS PROTEIN HAS HELICASE ACTIVITY.

-I- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS PROTEOLYTIC ACTIVITY.

-I- FUNCTION: WUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

-I- FUNCTION: WUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

-I- CATALYTIC ACTIVITY: Hydrolyzes glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1'

Liather vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLG PRSVH STANDARD; PRT; 3344 AA.

001901;

01-0CT-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: N·terminal protein (PI); Helper component proteinse (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2 (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NIA) (INIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein A (NI-A) (INIB) (RNA-directed RNA polymerase)
(EC 2.7.7.48); Coat protein (CP).
Papaya ringspot virus (strain P / mutant HA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang C.H., Bau H.J., Yeh S.D.; "Comparison of the nuclear inclusion b protein and coat protein genes of five papaya ringspot virus strains distinct in geographic origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93019006; PubMed=1402799; Yeh. S.D., Jan F.J., Chen M.C., Yeh. S.D., Jan F.J., Chiang C.H., Doong T.J., Chen M.C., Chung P.H., Bau H.J.; "Complete nucleotide sequence and genetic organization of papaya
PROSITE; PSS0096; 1Q; 2. Myosin; Calmodulin-binding; Repeat; Colled coil; ArP-binding; Repeat; Coiled coil; Alkylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 27; DB 1; Length 1471; 83.3%; Pred. No. 2.5e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  72 ATP (POTENTIAL).
88 ALKYLATION (BY SIMILARITY).
98 ALKYLATION (BY SIMILARITY).
169343 MW; E79C0FE72B041E95 CRC64;
                                                                                     MYOSIN HEAD-LIKE
                                                                                                               10 1.
10 2.
10 3.
10 4.
10 5.
COILED COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phytopathology 84:1205-1210(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ringspot virus RNA.";
J. Gen. Virol. 73:2531-2541(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                          824
849
849
928
1063
172
688
698
                                                                                                                                                                                                                                                          938 106
1299 140
165 17
688 68
698 69
1471 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and pathogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potyvirus.
NCBI_TaxID=31731;
                                                                                                                                                                                                                                                                                       DOMAIN
NP BIND
MOD RES
MOD RES
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                             DOMAIN
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POLG PRSVH
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Gin+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are
                                                                                                                                      (RNA)(N)

(ATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the processing of the potyviral polyprotein.

PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase; Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase; ATP-binding. 1 529 N-TERMINAL PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 kDa PROTEIN 2 (BY SIMILARITY).
GENOME-LINKED PROTEIN (BY SIMILARITY).
NUCLEAR INCLUSION PROTEIN A
                                                                                                              CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL PROTEINS.
SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
SIMILARITY: N.-A PROFIENASE BELONGS TO PEPTIDASE FAMILY C4.
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELPER COMPONENT PROTEINASE
(BY SIMILARITY).
PROTEIN P3 (BY SIMILARITY).
6 KDA PROTEIN I (BY SIMILARITY).
CYTOPLASMIC INCLUSION PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
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WUCLEAR INCLUGION PROTEIN B

(BY SIMILARITY).

COAT PROTEIN (BY SIMILARITY).

SIMILARITY).

SIMILARITY).

ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
E90CD7523AC5243D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR001450; Helicase C.
InterPro; IPR001450; Peptidase C4.
InterPro; IPR001592; Poty coat.
InterPro; IPR001592; Poty coat.
InterPro; IPR001265; RNA_Pol_PSP.
InterPro; IPR001095; RNA_Pol_PSP.
InterPro; IPR001095; RNA_Pol_PSP.
InterPro; IPR001095; RNA_Pol_PSP.
InterPro; IPR001095; RNA_Pol_PSP.
Pfam; PF00863; Peptidase C4; 1.
Pfam; PF00863; Peptidase C4; 1.
Pfam; PF00863; Peptidase C6; 1.
Pfam; PF00863; Peptidase C6; 1.
Pfam; PF00863; Peptidase C6; 1.
Pfam; PF00861; Peptidase C6; 1.
Pfam; PF00861; Peptidase C6; 1.
Pfam; PF00861; Peptidase C6; 1.
Pfam; PR00866; NNA_GP, RNA_DOI; 1.
PRNNTS; SN00467; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X67673; CAA47905.1; -.
EMBL; S46722; AAB23789.1; -.
EMBL; X67672; CAA47904.1; -.
PIR; JQ1899; JQ1899.
MEROPS; C04.009; -.
MEROPS; S30.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1493
1, 381040 N
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3344
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SPECIESE.COLI; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES=B.Coli; STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22389234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhew G.F., Donnenberg M.S., Blatner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence.
                                                                                                   Gape
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Nature 409:529-533(2001).
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SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V. Biley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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SPECIES=E.coli; STRAIN=C157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Bolinalanta E.T., Potamousis K
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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                                    Length 3344;
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                                                                                                   0; Indels
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yobf.
YOBF OR B1824 OR C2232 OR Z2869 OR ECS2534 OR SF1402.
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                    90.0%; Score 27; DB 1; I
83.3%; Pred. No. 6.1e+02;
ive 1; Mismatches 0;
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SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
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Escherichia coli 06,
Escherichia coli 0157:H7, and
                                                                                                      Conservative
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149 SVDLEY 154
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YOBF ECOLI
P76265;
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                                                                                                                                      "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.7%; Score 26; DB 1; Length 47; 100.0%; Pred. No. 11; 0; Mismatches 0; Indels
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EMBL, AE016701; AAA6891.1; -...
EMBL, AE005405, AAG5691.1; -...
EMBL, AE005588; BAB35957.1; -...
EMBL, AE015164; AAN43003.1; -...
EMBL, AE015164; AAN43003.1; -...
PIR, AE0794; R95794.
PIR, H64943; H64943.
R COGGMEN; EG14882; YobF.
HYDOLHeeical protein; Complete proteome.
SEQUENCE 47 AA; 5212 MW; 54E439F3331D700F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
HIJ323.
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RMSL, F3210895; AAG.

RMSSP, P15154; LE96.

DR InterPro; IPR001806; Ras trinsfrung.

DR InterPro; IPR001806; Ras trinsfrung.

DR InterPro; IPR002225; Small_GTP.

DR REdm, P700071; ras; 1.

DR SWART; SM00174; RHO; 1.

TO GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

19 122 GTP (BY SIMILARITY).

42 EFFECTOR REGION (POTENTIAL).

GERANYL-GERANYL, GRY SIMILARITY).

A42 EFFECTOR REGION (POTENTIAL).

GERANYL-GERANYL, GRY SIMILARITY).

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MEDLINE=21127961; PubMed=11222756;
Rivero F., Dielich H., Glocknef G., Noegel A.A.;
Rivero F., Dielich H., Glocknef G., Noegel A.A.;
The Dictyostellum discoldeum femily of Rho-related proteins.";
Nucleic Acids Res. 29:1068-1079(2001).
-1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
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Pred. No. 38;
2; Mismatches 0; Indels
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NCBI TaxID=44689;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RACI.
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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Best Local Similarity 66.7%;
Matches 4; Conservative 2
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PIR; H64025; H64025.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|:|
SLDIEY
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RACI DICDI
ID RACI DICDI
AC Q9GPR2;
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AAD16169.1;
BAB14399.1;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 SVEVEY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
TRFP_MOUSE
ID _TRFP_MOUSE
                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ROXO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crowley
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99134313; PubMed=9933582; Xiao H., Tao Y., Roeder R.G.; "The human homologue of Drosophila TRF-proximal protein is associated with an RNA polymerase II-SRB complex."; J. Biol. Chem. 274:3937-3940(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H., Wagatenma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Tayahasi T.;
Ninomiya K., Twayanagi T.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May regulate transcription of class II genes through association with the RNA polymerase II-SRB complex.
-!- SUBUNIT: Component of an RNA polymerase II-SRB complex.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                 Q9H944; O95821; Q9Y429;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
TRF-proximal protein homolog.
                                                                            212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 120-212 FROM N.A.
                                                                            STANDARD;
                                                                                                                                                                                                                                                           sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                          TRFP HUMAN
                       RESULT 20
TERP HUMAN

ID Q94944 HUMAN

ID Q94944 HUMAN

II 15-SEP

DT 15-SEP

DE TRF-Pr

CO COMMANDA

RA WATANA

RA ROBELIN

RA WATANA

RA RANA

RA RANA
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Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Sadarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Badarelli R., Kanapin A., Matsuda H., Batalov S., Beisel K. W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Madott D.R., Malteais L., Marchionni L., McKenzie L., Miki H.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Wanaz., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatuu N.,

RA Shiraki T., Waki K., Kawai J., Azawa K., Parkawa T., Fukuda S.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Milaning L.G., Wynnawal J., Azawa K., Parkawa T., Fukuda S.,

RA Shiraki T., Waki K., Kawai J., Azawa K., Parkawa T., Pukuda S.,

RA Milaning L., Wan Z., Zavolan M., Zhu Y., Zhakawa T., Pukuda S.,

RA Shiraki T., Waki K., Kawai J., Azawa K., Parkawa T., Rukuda S.,

RA Shiraki T., Waki K., Kawai J., Azawa K., Parkawa T., Rukuda S.,

RA Shiraki T., Waki K., Kawai J., Azawa K., Brakawa T., Fukuda S.,

RA Shiraki T., Waki K., Sasaki D., Shibata K., Shinagawa I.,

Ra Shiraki T., Waki K., Sasaki D., Shibata K., Shinagawa I.,

Ra Shiraki T., Waki K., Sasaki D., Shibata K., E., Rogere J.,

Ra Shiraki T., Parki K., Kaya W., Marefetton R., Lander B.S., Rogere J.,
EMBL; AK022092; BAB14399.1; ...
EMBL; AK022092; BAB14399.1; ...
EMBL; AL050196; CAB4314.1; ...
GO; GO:0016251; F:general RNA polymerase II transcription factor; TAS.
GO; GO:0005515; F:protein binding; TAS.
GO; GO:0005515; P:regulation of transcription from Pol II pro. . .; TAS.
Transcription regulation; Nuclear protein.
CONFLICT 134 136 SAR -> VP (IN REF. 1).
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 1; Length 212;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN REF. 1).
SAA7A39981EB1498 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
TRF-proximal protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              206 207 M
212 AA; 23222 MW;
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HEM3 AERPE
Q9Y9JO;
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CARBOHYD
CARBOHYD
SEQUENCE
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HEM3_AERPE
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RC STRAINE-CV. Columbia,

RC STRAINE-CV. Columbia,

RA MILINE-2106720; PubMed=11130713;

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdonenech P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Oberier F.,

RA Wincker D., Drzonek H., Erfle H., Jordan N., Benes V.,

RA Wiedelmann R., Kranz H., Voss H., Folland R., Barndt F.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

Conrad A., Hornischer K., Kauer G., Lochnert T.-H., Nordsiek G.,

RA Conred A., Hornischer K., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Royarro P., Collado C., Perez-Perez A., Otterwaelder B., Duchemin D.,

RA Mannhaupt G., Rasse D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fulli C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fulli C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walter A., Casacubert J.,

RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Wenter J.C.,

RA Sasamoto S., Kimura T., Idabawa K., Kawashima K., Kishida Y.,

RA Sasamoto S., Kimura T., Idabawa R., Rawashima R., Kishida Y.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Watanabe A., Yamada M., Yabuda S.,
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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28-FEB-2003 (Rel. 41, Last annocation update)
28-FEB-2003 (Rel. 41, Last annocation update)
28-FEB-2003 (Rel. 41, Last annocation update)
Expansin-like 3 precursor (At-EXPL3) (Ath-ExpBeta-2.3).
EXPL3 OR AT3G45960 OR F16L2_107
Arabidopsia thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
                                                            Component of an RNA polymerase II-SRB complex (By
association with the RNA polymerase II-SRB complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Score 26; DB 1; Length 212; 83.3%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Nuclear protein.
SEQUENCE 212 AA; 23192 MW; 88B116D0A9764438 CRC64;
                                                                                       similarity).
SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ245617; CAB53514.1; -. EMBL; AXC43396; BAC31536.1; -. MGD; MGI:1929648; Trfp.
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                    similarity)
                                                               SUBUNIT:
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Q9LZT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ID EXL3 AR
DT 28-FEB DT 2
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable porphobilingen deaminase (EC 4.3.1.8) (PBG)
(Hydroxymethylbilane synthase) (HYBS) (Pre-uroporphyrinogen synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE-9310339; PubMed=10382966;
MEDLINE-99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyana A., Fukui S., Nagai Y., Nishijina K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-1- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE
"Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPANSIN-LIKE 3.

EXPANSIN-LIKE EG45.

EXPANSIN-LIKE CBD.

N-LINKED (GLCNAC.,.) (POTENTIAL)

N-LINKED (GLCNAC.,.) (POTENTIAL)
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Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5D8A2048FEA7C292 CRC64;
                                          Nature 408 820-822 (2000).

-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
-!- SIMILARITY: Contains ! expansin-like EG45 domain.
-!- SIMILARITY: Contains ! expansin-like CBD domain.
-!- DATABASE: NAME=EXPANSIN homepage;
WWW="http://www.bio.psu.edu/expansins/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007112; Expan_endogl.
InterPro; IPR007118; Expan_Lol_pl.
InterPro; IPR007118; Expan_Lol_pl.
InterPro; IPR007117; Expan_Lol_pl.
Pfan; PF01357; Pollen_allergen; 1.
PRNTS; PR01225; ExPANSNFAMY.
ProDom; PD002179; Expan_Lol_pl_C; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
Glycoprotein; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 147 EX
161 243 EX
99 N-102 102 N-263 AA; 28559 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL162459; CAB82820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desulfurococcaceae; Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
263
147
243
102
                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; T47536; T47536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 VDVEY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=56636;
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Mycoplasma pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 SIDVQY 246
                                                                                                                                                                                                                                                                                                       Complete proteome.
NP BIND 45
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ses 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae."
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
RUVB MYCPN
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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        CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)0 = hydroxymethylbilane + 4 NH(3).

hydroxymethylbilane + 4 NH(3).

CORACTOR: COVALENTLY BINDS A DIPYRROMETHANE COFACTOR TO WHICH THE PORPHOBILINOGEN SUBUNITS ARE ADDED (BY SIMILARITY).

PATHWAY: PORPHYIN DIGOYNICHEBIS by the C5 pathway; fourth step. SIMILARITY: BELONGS TO THE HMBS FAMILY.
HYDROXYMETHYLBILANE PREUROPORPHYRINOGEN IN SEVERAL DISCRETE STEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRATS-ATC 33530 / G-37;
STRATS-ATC 33530 / G-37;
STRATS-ATC 33530 / G-37;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fraser C.M., Gocayne J.D., White O., Sarlavage A.R., Sutton G., Kelley J.M.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Frictoman J.L., Waldman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Frictoman J.T., Utcerback T.R., Saudek D.M., Phillips C.A., Merrick J.M.
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: THE RUVA-RUPS COMPLEX IN THE PRESENCE OF ATP RENATURES CRUCIFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE, INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HOMOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE HOLLIDAY JUNCTION MIGRATION BY LOCALIZED DENATURATION AND REANNELING (BY SIMILARITY).
-!- SUBUNIT: FORMS A COMPLEX WITH RUVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 26; DB 1; Length 305; 100.0%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57C78EE934C2799B CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF039U0; rollowards.

Prodom; PR00151; PORPHBDMASE.

ProDom; PD002745; PORPHDbil deam; 1.

PROSITE; PS00533; PORPHOBILINOGEN DEAM; 1.

Porphyrin biosynthesis; Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RUVB OR MG359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No.
                                                                                                                                                                                                                                                               EMBL; AP000064; BAA81310.1; -.
PIR; F72456; F72456.
HSSP; P06983; 1PDA.
HAMAP; MF 00260; -; 1.
InterPro; IPR000860; Porphobil deam.
Pfam; PF01379; Porphobil deam.
Pfam; PF03900; Porphobil deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 AA; 33085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
Les 5; Conservative
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049425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: THE RUYA-RUYB COMPLEX IN THE PRESENCE OF ATP RENATURES CROIFORM STRUCTURE IN SUPERCOILED DNA WITH PALLINDROMIC SEQUENCE, INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HOMOLOGOUS RECOMBINATION. RUYAB IS AN HELICASE THAT MEDIATES THE POLLIDAY JUNCTION MIGRATION BY LOCALIZED DENATURATION AND REANNELING (BY SIMILARITY).
-1- SUBBNIT: FORMS A COMPLEX WITH RUYA.
                                                                                                                                                                                                    TIGR; MG359; -...
HAWAP: MF 00016; -; 1.

InterPro; IPR00359; AAA ATPase.
InterPro; IPR004605; RuvB.
Pfam; PR00046, AAA; 1.

TIGRFAMS; TIGR00635; ruvB; 1.

TIGRFAMS; TIGR00635; ruvB; 1.

DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
NCBI_TaxID=2104;
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STRAIN=AFTC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl B., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 26; DB 1; Length 307; 66.7%; Pred. No. 83; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL),
376E5138279E396C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUVE MYCPN STANDARD; PRT; 307 AA. P75242; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) PFBB-2003 (Rel. 41, Last annotation update) Holliday junction DNA helicase ruvB. RUVB OR MPNS36 OR MP306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 24:4420-4449(1996).
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InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                       45 52 AT
307 AA; 35000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000028; AAB95954.1; -.
                                                                                                                                                        EMBL; U39717; AAC71584.1; -.
PIR; G64239; G64239.
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EMBL;
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MEDLINE=21608551; PubMed=11743194;
Medline B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Mcodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,
Qurollo B., Goldman B., Vaudin M., Iartchouk O., Epp A., Liu F.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
I'Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CS8.",
Science 294.232-2326(201).
C. - FUNCTION: FLIM IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
SCIENCE 294.2321-2328(201).
C. - FUNCTION: FLIM IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
COP THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE
MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon D.,
InterPro; IPR003959; AAA ATPase centr.
InterPro; IPR004605; RuvB.
Pfam; PPR00004; AAA; 1.
TIGRPANS; AAA; 1.
TIGRPANS; TGR0035; ruvB; 1.
DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Pahmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97305159; PubMed=9161425;
Deakin W.J., Parker V.E., Loake G.J., Shaw C.H.,
"The Agrobacterium tumefaciens motor gene, moth, is in a linked cluster with the flagellar switch protein genes, fliG, fliM and
                                                                                                                                                                                                                     .
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                                                                                                                                                                                  DB 1; Length 307;
                                                                                                                                                                                                                     Indels
                                                                                                                          P (POTENTIAL).
B1947D0C7AFFAF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
FLIM on ATUGEL OF AGR C 987.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                    321 AA.
                                                                                                                                                                              86.7%; Score 26; DB
66.7%; Pred. No. 83;
iive 2; Mismatches
                                                                                                                              ATP
                                                                                                                            52 A1
35012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:2317-2323(2001).
                                                                                                                                                              Query Match
Best Local Similarity bo...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 189:139-141 (1997).
                                                                                                                                           307 AA;
                                                                                                                                                                                                                                                                                        241 SIDVQY 246
                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=176299;
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                                                                                                                                                                                                                                                       1 SVDVEY
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                                                                                                                                                                                                                                                                                                                                                                                FLIM AGRTS
(44457;
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           PLIM AGRIS
AGRIS
AGRIS
DT 28-FEB-
DE 28-FEB-
DE PLAGOL
GN AGRICODIN
OC Rhizobi
OC Agrib
OC Agrib
OC Agrib
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91335768; PubMed=1651597;
Upton C., Macen J.L., Schreiber M., McFadden G.;
"Myxoma virus expresses a secreted protein with homology to the necrosis factor receptor gene family that contributes to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor soluble receptor precursor (Protein T2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%; Score 26; DB 1; Length 321; 66.7%; Pred. No. 87;
                                                                                                                                                                                                                                                                                           PIR, D97427; D97427.
Interpro, IRROD43; SpoA.
Pfam; PF01052; SpoA; Chemotaxis, Inner membrane;
Chemotaxis, Flagella, Flagellar rotation, Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                        157 157 G -> C (IN REF. 1).
160 160 E -> V (IN REF. 1).
321 AA; 34633 MW; D944CAE218C2D7B9 CRC64;
SUBCELLULAR LOCATION: Inner membrane-associated. SIMILARITY: BELONGS TO THE FLIM FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                     EMBL; AE009025; AAL41578.1; ALT_INIT.
EMBL; AE007990; AAK86373.1; -.
                                                                                                                                                                                                               EMBL; U63290; AAC45322.1; -.
EMBL; U95165; AAB71781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 184:370-382(1991).
                                                                                                                                                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
CONFLICT 157
CONFLICT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AIDVEY 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leporipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M002L OR T2.
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P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=84194000; PubMed=6232608;
MEDLINE=84194000; PubMed=6232608;
Powlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
Potential basies for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                   EMBL; U36837; AAB52384.1; -.

R HSSP; P03017; 2REB.

R HAMAP, MF_00268; -; -;

R InterPro; IPR001553; RecA.

R InterPro; IPR00154; RecA; 1.

R Pfun; PF00142; RECA;

R PROMO142; RECA;

R PROSITE; PRO0329; RecA; 1.

R PROSITE; PS50162; RECA_1; 1.

R PROSITE; PS50162; RECA_2; 1.

R PROSITE; PS50162; RECA_3; 1.

R PROSITE; PS50162; RECA_3; 1.

R PROSITE; PS50163; RECA_3; 1.

R PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crabtree G.R., Kant J.A., "Organization of the rat gamma-fibrinogen gene: alternative mRNA splice patterns produce the gamma A and gamma B (gamma ') chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87174801, PubMed=3562236, Morgan J.G., Holbrook N.J., Crabtree G.R., Morgan J.G., Holbrook N.J., Crabtree G.R., Nucleotide sequence of the gamma chain gene of rat fibrinogen: conserved intronic sequences."; Nucleic Acids Res. 15:2774-2776(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26, DB 1; Length 341;
Pred. No. 93;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY).
; F9D4BCCCEA69EAB5 CRC64;
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01-PEB-1996 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Fibrinogen gamma chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 AA.

    -i- SIMILARITY: Belongs to the recA family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=83129318; PubMed=6897622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND 80 87 P
SEQUENCE 341 AA; 37177 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 31:159-166(1982).
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112 SLDIEY 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVDVEY 6
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MEDLINE=97251810; PubMed=9097419;

Advivey P., Kince A., Hill C., Fitzgerald G.F.;

MEDLINE=97251810; PubMed=9097419;

MEDLINE=97251810; PubMed=9097419;

I deartification of a recA homolog (recALP) on the conjugative lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence plasmid pNP40: evidence plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence plasmid pNP40: evidence plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence 
                                               Gaps
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NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                             TUMER-CYS 1.

TUBE-CYS 2.

TUBE-CYS 3.

TUBE-CYS 4.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 26; DB 1; Length 326; 66.7%; Pred. No. 89;
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Plasmid pNP40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RecA protein, plasmid (Recombinase A) (recalp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
send an email to license@isb-sib.ch)
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                                     EMBL; M95181; AAA46632.1; -.
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Best Local Similarity 60.7.,
A; Conservative
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149
185
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287 NVDIEY 292
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ID RECA LACLA
AC 059486;
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CARBOHYD
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CARBOHYD
CARBOHYD
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REPEAT
REPEAT
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Бb
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Gaps

; 0

463 AA

PRT;

STANDARD;

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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                     X STAIN=H3TRY;

X MEDLINE=98295987; PubMed=9634230;

X MEDLINE=98295987; PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A. Hornsby T., Jagels K., Stelton S., Squares S., Squares R., Stelton S., Squares R., Suston J.E., Taylor K., Whitehead S., Barrell B.G.;

A Butter S., Seeger K., Skelton S., Squares S., Squares R., Suston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
                                                                                          30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Glycyl-trNA synthetase (EC 6.11.14) (Glycine--tRNA ligase) (GlyRS)
GLYS OR RV2357C OR MT2426 OR MTCY27.23 OR MTCY98.26.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
TST TaxID=1773;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                 SYG MYCTU
065932;
  RESULT 30
SYG_MYCTU
                                                        SOM THE STATE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                          Name=Gamma-A;

Isoid=PO2600-2; Sequence=VSP 001538, VSP 001539;

ISOId=PO2600-2; Sequence=VSP 001538, VSP 001539;

MISCELLANBOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE
EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
AGGREGATION.
SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH BETA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH ALPHA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH BETA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH BETA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00514; FIRRIN AG C DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma; Alternative splicing; Signal.
SIGNAL 1 25
CHAIN 26 445
FIBRINOGEN GAMMA CHAIN.
DISULPID 34 34 INTERCHAIN (WITH GAMMA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (In isoform Gamma-A) / FTId=VSP 001539.
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SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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                                                                                          Event=Alternative splicing; Named isoforms=2;
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BY SIMILARITY.
                                                                                                                                       IsoId=P02680-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, J00733; -; NOT_ANNOTATED_CDS.
EMBL, J00734; -; NOT_ANNOTATED_CDS.
EMBL, X05860; CAA22289-1; -.
EMBL, X05861; CAA22289-1; -.
EMBL, X0137; AAA98626-1; -.
FIR, A90828; FGRTGA.
HSSP; POZ679; JFID.
Interpro; IPRO2181; Fibrinogen_C, FEmm, PRO0147; fibrinogen_C, FEmm; PRO0147; fibrinogen_C; 1.
SWART; SM00186; FBG; 1.
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                                                                                                                      Name-Gamma-B
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SEQUENCE
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+ glycyl-tRNA(Gly).
--- SUBUNIT: Homodimer (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01043; TRNASYNTHGIN.
TIGREAMB; TIGR00389; glyS_dimeric; 1.
PROSITE; PS50862; AA_TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52937 MW; E8BDCE20B65538F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 295208; CAB08466.1; --
EMBL, AE007082; AAK46720.1; --
EMBL; AE007082; AAK46720.1; --
HSSP; P55206; 1ATI.

TIGR; MT2426; --
TUGR; MT2426; --
TUB-CCULIST; KV2357c; --
HAMAP; ME 00253; -; INTERPRO; IPR004154; HGTP anticodon.
InterPro; IPR002315; TRNA-Synt_2D;
InterPro; IPR002315; TRNA-Synt_2D;
InterPro; IPR002315; TRNA-Synt_2D;
InterPro; IPR006195; ENNA-Ilgase_II.
Pfam; PF00129; HGTP_anticodon; I.
Pfam; PF00129; TRNA-Synt_2D;
DRTANG, PF00129; TRNA-SYNT_2D;
DRTANG, PF00159; TRNA-SYNT_2D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 AA;
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SEQUENCE 463 AA;
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Gaps

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86.7%; Score 26; DB 1; Length 445; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels

86.78;

5; Conservative

VDVEY 444

440

2 VDVEY 6

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Local Similarity

Query Match Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiamydia trachomatis "; Science 282:754-759(1998).
-!- CATALYITC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate + L-lysyl-tRNA(Lys).
-!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
-!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                      Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Lihher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysyl-trna synthetase (EC 6.1.1.6) (Lysine--trna ligase) (Lysrs)
LYSS OR CT781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- CATALYTIC ACTIVITY: L-arabinose = L-ribulose.
-1- PATHWAY: L-arabinose catabolism; first step.
-1- SIMILARITY: Belongs to the arabinose isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 1; Length 496;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR, TM0276; -.
HAMAP; MF 00519; -; 1.
HAMAP: MF 00519; -; 1.
InterPro; IPR003162; Lara isomerase.
Pfan; PF02510; Arabinose Isome; 1.
ProDom; PD018364; Lara isomerase; 1.
Prodom; PD018364; Lara isomerase; 1.
Isomerase; Arabinose catabolism; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                    SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001709; AAD35365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 86.7%;
Similarity 66.7%;
4; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B72398; B72398,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 AIDVEY 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYK_CHLTR
O84786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
SYK_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINTCI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Where complete sequence of the Pyrococcus furiosus genome.";
Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes amidations at positions B. D., E, and G on adenosylcobyrinic A,C-diamide. NH(2) groups are provided by glutamine, and one molecule of ATP is hydrogenolyzed for each amidation (By similarity).
-!- PATHWAY: Cobalamin biosynthesis.
-!- SIMILARITY: BELONGS TO THE COBB/COBQ FAMILY. COBQ SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
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0
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                                  Length 463;
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Pred. No. 1.38+02;
.::-marrhes 0; Indels
                              86.7%; Score 26; DB 1; Length 463
66.7%; Pred. No. 1.38+02;
cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP, M. 00028, -; 1.
HAMAP, M. 00028, -; 1.
INTERPRO, IPR002586; CbiA.P.
InterPro; IPR004459; CobQ.
Pfam; PF01656; CbiA; 1.
TIGRPAM; TIGR00313; CobQ; 1.
Cobalamin biosynthesis; Complete proteome.
Cobalamin biosynthesis; Complete proteome.
Cobalamin biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Probable cobyric acid synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAA_THEMA STANDARD; E Q9WYB3; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seques 28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE010154; AAL80425.1; -.
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Query Match
Best Local Similarity 66.79,
A; Conservative
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Best Local Similarity 66...
4, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus.
                                                                                                                                                                                                                                 268 TVDIEY 273
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471 SIDVDY 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                   1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2261;
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QBU3Z8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus
                                                                                                                                                                                                                                                                                                                                                           COBQ_PYRFU
ACOBQ_PYRFU
ACOBQ_PYRFU
ACOBQ_PYRFU
ACOBG OR ACOBG OR ACCOBG OR ACCOBC OR A
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DT 28-FEB
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ö Gaps . 0 86.7%; Score 26; DB 1; Length 526; 83.3%; Pred. No. 1.5e+02; iive 1; Mismatches 0; Indels Best Local Similarity 83.3 Matches 5; Conservative

||:||| SVEVEY 7 1 SVDVEY 6 Š

STANDARD; UVRC MYCBV 084898;

Mycoplasma bovis. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. SEQUENCE FROM N.A. NCBI_TaxID=28903;

STRAIN=PG45; MEDLINE=98329280; PubMed=9664578;

Nabel Manager Strong Function of Wordplasma bovis and Mycoplasma agalactiae Species identification of Mycoplasma bovis and Mycoplasma agalactiae based on the uvrC genes by PCR."

1. FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrC both incises the 5' and 3' sides of the lesion. The N-terminal half is responsible for the 3' incision and the C-terminal half is responsible for the 5' incision (By similarity).

1. SUBUNIT: Interacts with uvrB in an incision complex (By

similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the uvrc family.
--- SIMILARITY: Contains 1 UVR domain.

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ö (See http://www.isb-sib.ch/announce/ Gaps | HAMAP, WF 00203; ALCOSONIA, ALC .. 0 1; Indels SEQUENCE 571 AA; 66463 MW; 717DA202CA50DCE3 CRC64; 86.7%; Score 26; DB 1; I 83.3%; Pred. No. 1.6e+02; 0; Mismatches entities requires a license agreement (Se or send an email to license@isb-sib.ch). SAR EMBL; AF003959; AAC32309.1; Local Similarity 83.3 nes 5; Conservative 219 409 SADVEY 414 1 SVDVEY 6 184 Query Match DOMAIN ઠ 임

STANDARD; ACE HABIE Q10715;

Haematobia irritans exigua (Buffalo fly). Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Fterygota; Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia. 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-RDB-2003 (Rel. 41, Last annotation update)
Anglotenain-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl carboxypeptidase I) (Kininase II). NCBI_TaxID=34678;

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Mech. Dev. 51:157-168(1995).

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Cornell M.J., Coates D., Isaac R.E.;
"Characterisation of putative Drosophila angiotensin converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Canton-S;
MEDLINE=96028519; PubMed=7547464;
Tatel K., Cai H., Ip Y.T., Levine M.;
"Race: a Drosophila homologue of the angiotensin converting enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornell M.J., Williams T.A., Lamango N.S., Coates D., Corvol P., Soubrier F., Hoheisel J., Lehrach H., Isaac R.E.; Cloning and expression of an evolutionary conserved single-domain angiotensin converting enzyme from Drosophila melanogaster."; J. Biol. Chem. 270:13613-13619(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidy) carboxypeptidase I) (Kininase II). ANCE OR RACE OR BG:DS08220.3 OR CG8827.
                                                                                                                                 InterPro; IPR001548; Peptidase M2.
InterPro; IPR006025; Zn MTpepdse.
Pfan; PF01401; Peptidase M2; 1.
PROMYS; PR00791; Peptidase M2; 1.
ProDom; PD004184; Peptidase M2; 1.
PROSITE; PS001142; Z1NC_PROTEASE, 1.
Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase; Glacin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                        368 BY SINILARITY.
371 ZINC (CATALYIC) (BY SIMILARITY).
53 N-LINKED (GLCNAC. .) (POTENTIAL).
196 N-LINKED (GLCNAC. .) (POTENTIAL).
70505 MM; A43D6DF5A83ECB53 CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota, Merazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 1; Length 611;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACE_DROME STANDARD; PRT; 615 AA. 010714; 027572; 09NE4; 09TX66; 09VJV3; 01-NOV-1997 (Rel. 35, Created) PFEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
  send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Soc. Trans. 21:243-243(1993).
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                                                   EMBL; L43965; AAA70427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
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368
371
                                                                                      PIR; S65472; S65472.
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196
531
611 AA;
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ses 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    367
368
371
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                                                                                                          MEROPS; M02
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RATAIN-BERKELEY,

RA Adams M.D., Celniker S.E., Li P.M., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.M., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Button G.G., Wortman J.R., Easter R.G., Change M., Miklos G.L.G.,

RA Abril J.F., Appayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Bacchan M.R., Bouck J., Bottler P., Brottler P.,

RA George R.C., Busam D.A., Buller H., Cadieu E., Cener A., Cener A.,

Burtis K.C., Busam D.A., Ballke C., Davenport L.B., Davies P., M.

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., M.

Burtis K.C., Busam D.A., Buller C., Perraz C., Perriac S., Dunkov B.C., Dun P.,

RA Dodson K., Doup L.B., Downes M., Dagan-Rocha S., Dunkov B.C., Dun P.,

RA Dodson K., Doup L.B., Downes M., Dayan-Rocha S., Dunkov B.C., Dun P.,

RA Dodson K., Doup L.B., Downes M., Glabart W.M., Glasser K.,

RA Gerer J.M., Gang F., Gorrell J.H., Gu Z., Ganan P., Harris M.,

RA Harris N.L., Hervey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Hervey D., Heiman T.J., Hernandez J.R., Machelison D.L.,

RA Harris N.L., Mattor S.D., Mornary C., Morris J., Moshrefi A.,

Rabardon M., Pittenna N.Y., Mobarry C., Morris J., Moshrefi A.,

Rabardon K.A., Moy M., Murphy B., Weller S., Stoeller F., Shen H.,

Rabier E., Spadling A.C., Stapleron M., Strong R., Suche B.,

Rabier E., Spadling A.C., Stapleron M., Strong R., Waller S., Randers R., Wenter J., Wang S., Yang S., Zhan M., Waller S., Waller S., State S., State S., State S., State S., State S., Stat
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SUBCELDULAR LOCATION: Extracellular DEVELOPMENTAL STAGE: EXPRESSED IN THE AMNIOSEROSA DURING GERM BAND ELONGATION, SHORTENING AND HEART MORPHOGENESIS. EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BERKELEY; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNa resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-1- FUNCTION: MAY PLAY A ROLE IN THE CONTRACTIONS OF THE HEART, GUT
                                                                                                                Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R.G., Davis T., Doyle C., Galle R.F., George R.A., Harris N.L., Harrizell G., Harvey D., Hong L., Houston K.A., Hoskins R.A., Johnson G., Martin C.H., Moshrefl A., Palazzolo M., Reese M.G., Spradling A.C., Tsang G., Wan K.H., Miltelaw K., Celniker S.E., Rubin G.M.; an exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                                                                                            MEDLINE=99403001; PubMed=10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                     Genetics 153:179-219(1999)
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fission yeast.";
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                 EMBL; U25344; AAB02171.1; -...

DR EMBL; U34599; AAC46902.1; -...

DR EMBL; AE003461; AAC46902.1; -...

DR EMBL; AE003461; AAC4834.1; -...

DR EMBL; AE003461; AAC28677.1; -...

DR EMBL; AC06129; AAL28677.1; -...

DR FIYBASS; FBGT0012037; Ance.

DR GO, GO: 0002466; F:peptidate M2.

DR InterPro; IPR00148; Peptidase M2.

DR FRINTS; PR00791; PED1PTASEA.

DR PRINTS; PR00791; PED1PTASEA.

DR PROSITE; PS00142; ZINC PROTEASE; 1...

PROSITE; PS00142; ZINC PROTEASE; 1...

PHYDROLEN; SIGNAL

BRINTS; SIGNAL

DR DACACCECTION PROTEASE; 1...

DR DACOPORTEDING SIGNAL

BRINTS; SIGNAL

DR DACOPORTEDING SIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=21534324; PubMed=11676924;
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SIC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.7%; Score 26; DB 1; Length 615; 83.3%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70926 MW; 9E3F9A41C51B9485 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIL SCHPO STANDARD; PRT; 693 AA. 096TL7; Q9UTN1; Q9UU15; 28-FB3-2003 (Rel. 41, Created) 28-FB2-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) DNA-binding protein rapl. BARL OK SPECTY78.02. Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
  MIDGUT THROUGHOUT EMBRYOGENESIS
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es 5; Conservative
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402
414
486
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DT 08-FEB-

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ARAILE 21849401; PubMed=11859360;

RA MEDLINE=21849401; PubMed=11859360;

RA MOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sayouros U., Feat, N., Hayles J., Basham D., Bowman S., Brooks K., Brown D., Hariss D., Hidalgo D., Hodgson G., A Gonlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., A Gentles S., Goble A., Hamlin N., Harriss D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarths S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Hornsby T., Howarths S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Squares M., Seeger K., Sharp S., Relton J., Simmonds M., Squares R., Squares S., Stevens K., A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Ry Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Ry Jork M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., A Eger P., Zimmermann W., Wedler H., Wanbutt R., Purnelle B., Gaffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Romaniguez A., Revuelta J.L., Moreno S., Ammstrong J., Forsburg S.L., A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Rh Gerrutti L., Lowe T., MocCombie W.R., Paulsen I., Powe P.; Maring Bord, Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Involved in the regulation of telomere length, clustering and has a specific role in telomere position effect (TPE). Unlike yeast, exhibits now effect in transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                          "spRapl and spRifl, recruited to telomeres by Tazl, are essential for telomere function in fission yeast.";
Curr. Biol. 11:1624-1630(2001).
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Chikashige Y., Hiraoka Y.; "Telomere binding of the Rapl protein is required for meiosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT MEDLINE=21534325; PubMed=11676925;
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STRAIN-968 h90;
MEDLINE-20223868; PubMed=10759889;
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                                                                                                                                                                   Biol. 11:1618-1623(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                            Kanoh J., Ishikawa F.;
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DEVH BOX
                                                                                                                                           EMBL; 299115; CAB14139.1; --
PIR; B65941; B65941.
Subtinist; B011451; yprA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Hellcase_C.
Pfam; PF00270; DEAD;
Pfam; PF00271; helicase_C; 1.
                                                                                                                                EMBL; L47838; AAB38468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-551 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                           SMART; SM00487; DEXDC; T. SMART; SM00490; HELICC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                          749 AA;
                                                                                                                                                                                                                                                                                                             Complete proteome.
NP BIND 76
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P59470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis chromosome region between
the serA and kdg loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                ..
0
                                                                                             Score 26; DB 1; Length 693;
Pred. No. 2e+02;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                               79526 MW; 77C5070697D1A9CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Putative helicase yprA.
                                                                                                                            2; Mismatches
InterPro, IPR001357; BRCT.
PROSITE; PS50172; BRCT; 1.
DNA-binding; Telomere; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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MEDLINE=96349105; PubMed=8760912;
                                                 BRC
                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
                                                                                           Match 86.7%;
Local Similarity 66.7%;
hes 4; Conservative ;
                                                                                                                                                                                                                                                                          STANDARD;
                                                               693 AA;
                                                                                                                                                                              |:||:|
249 SIDVDY 254
                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                              1 SVDVEY 6
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PS0830;
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                                                                SEQUENCE
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                                                                                              Query Match
                                                DOMAIN
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RY SEQUENCE OF 1-5:51 FYCUM NA.

RY SUDENCE STRAIN-657BL/681:

RA OKAZAKI Y., FUTUDO M., KASUKAWA T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., OSATO N., Salto R., Buzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Brust V., Chochia C., Corbani L.E., Cousins S.,

RA Dalla B., Dragani T.A., Fletcher C.F., Forrest R., Frazer K.S.,

RA Gasteriand T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawaswa Y., Kedaierski R., King B.L.,

RA Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Ravasi T., Reed D.J., Reid J., Ring B.S., Ringwald M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Sakazume N., Sato K.,

RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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0
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 1; Length 749;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Hydrolase; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84589 MW; 3F653EFA8EC3A7EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY).
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                          STRAIN=K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Man B., Shao Y.;
                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
   16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yliE.
YLIE OR B0833.
                                                                                                                                                                                                                                                                       MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
                                                      Escherichia coli
                                                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                                                            STRAIN=K12
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                             {RNA}(N).
-!- SUBUNIT: RNA polymerase III consists of about 15 different
subunits. This subunit is the second largest component of RNA
polymerase III (By similarity)
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BC044796; AAH44796.1; -.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Zinc-finger; Nuclear protein.
ZNC-finger; Nuclear protein.
C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%; Score 26; DB 1; Length 756
66.7%; Pred. No. 2.2e+02;
wismarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703 718 C4-TYPE (FOLDALLIL).
551 552
756 756
756 AA; 85062 MW; 336763B7CEBBAFB8 CRC64;
                                                                                                     SEQUENCE OF 552-756 FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK039366; BAC30327.1; -.
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Best Local Similarity 66.,
4, Conservative
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Anger thankstrad Towns

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"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
-1- SIMILARITY: Contains 1 EAL domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 782 AA, 90048 MW, 608DFB0068611DFB CRC64;
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83.3%; Pred. No. 2.3e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRE-2003 (Rel. 41, Last annotation update)
POLB OR APEZ098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50883; EAL; 1.
Hypothetical protein; Complete proteome.
DOMAIN 527 781 EAL.
                                                                                                                                                                                                                                                                                      EMBL; AE000185; AAC73920.1; --
EMBL; D90721; BAA35536.1; --
PIR; A64821; A64821.
EcoGene; EG13476; yliE.
ThterPor, IPR001633; EAL.
Pfam; PF00563; BAL; 1.
SWART; SM00052; DUF2; 1.
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Best Local Similarity 83.3.
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ID DPO2_AERPE
AC 093746;
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782 AA.

PRT;

RESULT 40
YLIE ECOLI
1D YLIE ECOLI STANDARD; 1
D 72 P75800;
DT 16-OCT-2001 (Rel. 40, Created)

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MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

ABO Q., Tian Y., Lia Y., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

ABO Q., Tian Y., Lia Y., Lu X., Huang L., Dong X., Ma Y., Ling L.,

A Chen Y., Xue Y., Xu Y., Lat X., Huang L., Dong X., Ma Y., Ling L.,

A Chen Y., Xue Y., Xu Y., Lat X., Huang L., Dong X., Ma Y., Ling L.,

A Complete Sequence of T., tengcongensis genome.";

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC SETION: Cytoplasmic.

C CATALYTY: Belongs to the phenylalanyl-tRNA synthetase beta chain

C C CATALYTY: Contains 1 tRNA-binding domain.
                                Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PheRS).
PHBT OR TTE1689.
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457
463
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467 4
794 AA;
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457
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                                                                                                                                                              STRAIN=K1;
Ishino Y., Cann I.K.;
"Isolation of the genes encoding two alpha-like DNA polymerases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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KIGERVILEWWOIG -> R (IN REF. 1).

E. > Q (IN REF. 1).

IRILQY -> SAHTSSN (IN REF. 1).

T. > I (IN REF. 1).

T. > I (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB017501; BAA75663.1; -...

EMBL; AB017501; BAA75663.1; -...

HISP, P56689; 1750.

InterPro; IPR006172; DNA_DOl_B -...

InterPro; IPR006134; DNA_DOl_B -...

InterPro; IPR004133; DNA_DOl_B -...

InterPro; IPR004578; Pol_Z -...

InterPro; IPR004578; Pol_Z -...

InterPro; IPR004678; Pol_Z -...

InterPro; IPR004678; Pol_Z -...

InterPro; IPR004678; Pol_Z -...

InterPro; IPR004678; Pol_Z -...

InterPro; IPR00486; Pol_B -...

InterPro; INTR00592; Pol_Z -...

InterPro; INTR00592; Pol_Z -...

InterPro; INA_directed DNA_Pol_Ymerase; DNA_replication;
                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 26; DB 1; Length 784; 100.0%; Pred. No. 2.38+02; ive 0; Mismatches 0; Indels
 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                       Aeropyrum pernix.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89639 MW;
              Desulfurococcaceae; Aeropyrum.
NCBI_TaxID≥56636;
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Best Local Similarity 100...
From 5, Conservative
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355
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763
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784 AA;
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                                                    SEQUENCE FROM N.A.
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CONFLICT
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SYFB THETN
Q8R9C7;
15-SEP-2003
15-SEP-2003
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CONFLICT
SEQUENCE
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SYFB THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Metal-binding; Magnesium; RNA-binding; tRNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MAGNESIUM (VIA CARBONYL OXYGEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
F9179929B0461A7F CRC64;
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VP3 BTV10
ID VP3 BTV10
STANDARD; PRT; 901 AA P12435;
DT 01-0CT-1989 (Rel. 12, Created)
DT 01-0CT-1989 (Rel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRNA-BINDING.
                                                                                                                                                                                                                                                                 HAMAP; MF_00283; -; 1.
InterPro; IPR005146; B3 4.
InterPro; IPR005147; B5 4.
InterPro; IPR005121; Rdx-AntiCB.
InterPro; IPR004532; PheT_bact.
InterPro; IPR004532; PheT_bact.
InterPro; IPR004532; PheT_bact.
Fam; PP03484; B5; 1.
Pfam; PP03484; B5; 1.
Pfam; PP031889; TRNA_bind; 1.
IGRFAM9; IIGR0472; pheT_bact; 1.
Pro; IPR05188; TRNA_bind; 1.
                                                                                                                                                                                                                                            EMBL; AE013123; AAM24889.1; -.
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Query Match
Best Local Similarity 100....
Best Local Si Conservative
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(Rel. 42, Created) (Rel. 42, Last sequence update) (Rel. 42, Last annotation update)

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SEQUENCE FROM N.A.
MEDLINE=94360628; PubMed=8079518;
                                                                                                                                                                                                                                 InterPro; IPR002614; Orbi VP3.
Pfam; PF01700; Orbi VP3; I.
ProDom; PD004438; Orbi VP3; I.
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Pfam; PF01700; Orbi VP3; 1.
ProDom; PD004438; Orbi VP3; 1.
                                                                                                                                                                                  EMBL; L19968; AAA42846.1; -. HSSP; P56582; 2BTV.
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Best Local Similarity 66.7%
Matches 4, Conservative
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454 TIDVEY 459
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SEQUENCE 90
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VP3 BTV13
ID VP3 BTV13
AC Q65750;
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                                                                                                                                                                                                                                                                                                                  (2) SEQUENCE FROM N.A.

MEDLINE-90345726; PubMed=2166648;

Roy P., Marshall J.J.A., French T.J.;

"Structure of the bluetongue virus genome and its encoded proteins.";

Curr. Top. Microbiol. Immunol. 162:43-87(1990)

-!- FINCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.

-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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SEQUENCE FROM N.A.
MEDLINE-94360628; Pubmed=8079518;
MEDLINE-94360628; Pubmed=8079518;
Hwang G.-Y., Xiang M., Li J.K.-K.;
"Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses.";
virus Res. 32:381-389(1994).
-!- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
                                                                                                                                                                                MEDLINE=86046560; PubMed=2998117;
Ghiasi H., Purdy M.A., Roy P.;
"The complete sequence of bluetongue virus serotype 10 segment 3 a
its predicted VP3 polypeptide compared with those of BTV serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 AA; 103342 MW; 4E485F5A38FC6456 CRC64;
                                                            Bluetongue virus (serotype 10 / isolate USA).
Viruses, dsRNA viruses, Reoviridae, Orbivirus.
NCBI_TaxID=10900;
15-DEC-1998 (Rel. 37, Last annotation update) VP3 core protein (Major inner capsid protein)
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP3 core protein (Major inner capsid protein)
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InterPro, IPR002614, Orbi_VP3.
Pfam, PF01700, Orbi_VP3, 1.
ProDom; PD004438, Orbi_VP3; 1.
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                                                                                                                                                                                                                                                                                                  Virus Res. 3:181-190(1985)
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454 TIDVEY 459
                                                                                                                                        [1]
SEQUENCE FROM N.A.
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SEQUENCE 90
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VP3 BTV11
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Matches
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VP3 BIV11
VP3 BIV11
VP3 BAC Q6574
DT 15-DE DT 1
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"Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses.";
Virus Res. 32:381-389(1994).
-!- FUNCTION: THE VPS PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 1; Length 901; 66.7%; Pred. No. 2.6e+02; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 AA; 103405 MW; 2C81F5D7CA304D0D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bluetongue virus (serotype 13 / isolate USA).
Viruses, dsRNA viruses, Reoviridae, Orbivirus.
NCBI_TaxID=33717,
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
13-DEC-1998 (Rel. 37, Last annotation update)
33 OR L3.
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X. RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

X. REDLINE-98445087; PubMed=9774103;

X. ADLINE-98445087; PubMed=9774103;

X. ADLINE-98445087; PubMed=9774103;

X. Zientara S., Merrens P.P., Stuart D.I.; Guet P., Diprose J.M., Malby R.,

Zientara S., Merrens P.P., Stuart D.I.; Guet P., Diprose J.M., Malby R.,

X. Zientara S., Merrens P.P., Stuart D.I.; Mature 395:470-478(1998).

X. The atomic structure of the bluetongue virus core.";

X. Mature 395:470-478(1998).

X. L. FUNCTION: THE VPR PROTEINS (WITH VPI, VP4, VP6 AND VP7) WHICH FORM THE INNER CABBID OF THE VIRUS.

X. C. I. SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.

PDB; 2BTV; 09-288P-98.

X. InterPro; IPR002614; Orbi_VP3; I.

X. R. R. Pfam; PF01700; Orbi_VP3; I.

X. Core protein; 3D-structure.

X. TURN.
              orbivirus isolates.";
Virus Res. 7:169-183(1987).
-!- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!- SIMILARITY: BELONGS TO THE RECVIRUSES VP3 FAMILY.
HSSP; P56582; 2BTV.
InterPro; IRR002614; Orbi VP3.
Ffam; PF01700; Orbi VP3; 1.
South Africa and the United States of America, and with other
                                                                                                                                                                                                                                                                                                          86.7%; Score 26; DB 1; Length 901; 66.7%; Pred. No. 2.6e+02; ive 2; Mismatches 0; Indela
                                                                                                                                                                                                                                                                901 AA; 103205 MW; 12312208188C1206 CRC64;
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Viruses; dsRNA viruses; Reoviridae; Orbivirus.
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
VP3 core protein (Major inner capsid protein)
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Best A; Conservative
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454 TIDVEY 459
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SEQUENCE 9
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P56582;
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VP3_BTV1S
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=85242823; PubMed=2989873;
MEDLINE=85242823; PubMed=2989873;
Roy P., Purdy M.A., Petre J., Rao C.D.;
"Cloning and nucleotide sequencing of bluetongue virus genomes.";
Prog. Clin. Biol. Res. 178:363-370(1985).
-I- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-I- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 PAMILY.
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Viruses, dsRNA viruses; Reoviridae; Orbivirus.
NCBI_TaxID=10904;
                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                         VP3 core protein (Major inner capsid protein)
S3 OR L3.
                                                                                                                                                                                                       Bluetongue virus (serotype 17 / isolate USA).
Viruses; dsRNA viruses; Reoviridae; Orbivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VP3 BTV1A STANDARD; PRT; 901 AA. 220608 | PEB=1991 (Rel. 17, Created) 01-FEB=1991 (Rel. 17, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 33 core protein (Major inner capsid protein) 53 OR L3.
                                         901 AA
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=84292453; PubMed=6206235;
Purdy M.A., Petre J., Roy P.,
"Cloning of the bluetongue virus L3 gene.";
J. Virol. 51:754-759(1984).
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002614; Orbi VP3.
Pfam; PF01700; Orbi VP3; I.
ProDom; PD004438; Orbi_VP3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; K02369; AAA42831.1; -.
EMBL; M32722; AAA42839.1; -.
PIR; A04148; P3XR17.
HSSP; P56582; 2BTV.
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Best Local Similarity 66...
For 4; Conservative
                                         STANDARD;
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                                                                                                                                                                                                                                                      NCB1_TaxID=33718;
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                                       VP3_BTV17
P03539;
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RESULT 47
VP3 BTV1A
DD P236
DT 01-FE
DT 01-FE
DT 15-DE
DE VP3 C
GN S10R
OX NCB1
RX MEDL1
RX MEDL1
RT and ¢

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FT TURN 196 197
FT STRAND 202 204
FT HELIX 212 226
FT TURN 246 245
FT TURN 266 245
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FT TURN 266 246
FT STRAND 263 266
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FT TURN 346 346
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FT TURN 569 659
FT TURN 569 659
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FT TURN
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MEDLINE=94360628; PubMed=8079518;

Hwang G.-Y., Xiang M., Li J.K.-K.;

Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses.";

Virus Rse. 32:381-38911994).

-!-FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.

-!-SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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86.7%; Score 26; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.7%; Score 26; DB 1; Length 901; Best Local Similarity 66.7%; Pred. No. 2.6e+02; Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103181 MW; B89384F344AE3669 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 49
VP3 BTV2A

AC 065748;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DF 15-DEC-1998 (Rel. 37, Last sequence update)
DF 072 COTE protein (Major inner capeid protein).
OS NR L3.
OS NR L3.
OS L3.
OYIUNGE GRANA WITUSES; Recviridae; Orbivirus.
OX NCBI_TAXID=10907;
RN MEDLINE=94360628; PubMed=8079518;
RN WEDLINE=94360628; PubMed=8079518;
CC the five United States bluetongue viruses.";
Virus Res. 32:381-389(1994).
CC -1 FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE
CC -1 FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE
CC -1 FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE
CC -1 FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE
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1133 AA.

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STANDARD;
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454 TIDVEY 459
1 SVDVEY 6
                     Hernandez N.;
      HUMAN
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(3)
SEQUENCE OF 751-1133 FROM N.A.
SEQUENCE OF 751-1133 FROM N.A.
SA SUBJECT CARCIONMA, S. SUGIYAMA T., Otsuki T., Suzuki Y.,
SA Nishikawa T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
Magatsuma M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Cono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Namancto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RD human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC --- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC --- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription TISSUENCE FROM N.A.

TISSUE-Muscle;

MEDLINE-2388257; PubMed=12477932;

Altschul S.C., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang D., Haibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raplecon M., Soares M.B., Bonaldo M.F., Carannon R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rockwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nillalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Nilling M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakealey R. W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length "Characterization of human RNA polymerase III identifies orthologues for Saccharomyces cerevisiae RNA polymerase III subunits."; Mol. Cell. Biol. 22:8044-8055(2002). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 15-SEP-2003 (Rel. 42, Created) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) DNA-directed RNA polymerase III subunit 127.6 kDa polypeptide FCC 2.7.7.6) (RNA polymerase III subunit 2) (RPC2) SEQUENCE FROM N.A. MEDLINE=22278866; PubMed=12391170; Hu P., Wu S., Sun Y., Yuan C.-C., Kobayashi R., Myers M.P., U.S.A. 99:16899-16903(2002). Proc. Natl. Acad. Sci.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate {RNA}(N).
SUBUNIT: RNA polymerase III consists of about 15 different
subunits. This subunit is the second largest component of RNA

polymerase III. SUBCELLULAR LOCATION: Nuclear

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Search completed: January 20, 2004, 13:55:20 Job time : 13 Becs

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BMBL, BC046238; AAH46238.1; -.
BMBL, AK001256; BAA91581.1; ALT_INIT.
BMBL, AK001256; BAA91581.1; ALT_INIT.
InterPro; IPR01572; RNA_pol_RDL_0.1
Pfam; PF004562; RNA_pol_RDDL_7; 1.
Pfam; PF04566; RNA_pol_RDDL_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; DNA_directed RNA_polymerase; Transcription; Zinc; .. Length 1133; 1080 1095 C4-TYPE (POTENTIAL). 258 258 E -> A (IN REF. 1). 978 978 R -> C (IN REF. 3; BAA91527) 1133 AA; 127784 MW; FOB3AFF892DDED7D CRC64; 0; Indels 86.7%; Score 26; DB 1; I 66.7%; Pred. No. 3.3e+02; 2; Mismatches Zinc-finger; Nuclear protein. ZN FING 1080 1095 CONFLICT 258 258 Conservative 114 TVDIBY 119 Query Match Best Local Similarity 1 SVDVEY 6 4, SEQUENCE CONFLICT Best Loc Matches STITE WE BEAR BEAR SOLUTION OF THE SOLUTION OF 셤 ò

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Q9fgn0 arabidopsis
Q8fil36 plasmodium
Q21492 caenorhabdi
O52373 caldicellul
O8mmk4 dicryosteli
Q8mcx2 pseudomonas
Q9adw6 ehrlichia c
Q8fu72 corynebacte
Q8v3p9 swinepox vi
Q23355 caenorhabdi
O12337 marek's dis
Q9u3g5 caenorhabdi
O12337 marek's dis
Q9u3g5 caenorhabdi
O12337 marek's dis
Q9x2g8 escherichia
Q8x2b1 subobacteri
Q47903 fusobacteri
Q47903 fusobacteri
Q47903 fusobacteri
Q47903 fusobacteri
Q47903 fusobacteri
Q8x4c8 escherichia
Q8x4c8 escherichia
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Q9FGN0
Q81L36
Q27492
O52373
Q8MMK4
Q8SCX2
Q9ADW6
Q8FU72
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Q9U3Q5
Q12377
Q09968
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Q8HJ75
Q8K298
Q8K298
Q8K298
Q8LGS6
Q99JFS
Q8DK73
Q9DJFS
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Q9DJFS
Q8DFS
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Q8F157
Q9RP94
Q8T0R9
Q9JXR3
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Q9JXR3
Q8J1248
Q80245
Q8FEX7
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Q8YF57;
Q8YF57;
Q1-MAR-2002 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
01-JUN-2002 (TrEMBLrel. 21
Arsenate reductase.
BMEI1670.
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Q8g999 medicago sa
Q55284 streptococc
Q25177 bydra atten
Q8p613 xanthomonas
Q8p613 xanthomonas
P93125 dunaliella
Q9nfr4 drosophila
Q9nfr4 coorpridiu
Q97567 caenorhabdi
Q97684 clostridium
Q8cwf5 wiggleswort
Q8wf5 aplysta cal
Q9961 arxula aden
Q9961 arxula aden
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(without alignments)
43.009 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 75 summaries
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Q8GZR4
Q9899
Q53284
Q25177
Q8FHD3
Q8FD3
Q9DSP4
Q9L5P9
Q9CSP67
Q8CWIF
Q8CWIF
Q8CWIF
Q8WSF9
Q9MSF9
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sp_bacteria:*
sp_human:*
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sp_nammal:*
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sp_organelle:*
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                                                                      protein search,
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Perfect
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No.
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Rosidae;

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A Brill L.M., Pleternel V.R.;

"Legume seed lectin genes: sequence of Mslec2 from Alfalfa, Alfalfa
and Sweet Clover souther: bloc analysis, and stable transformation of
and Sweet Clover souther: bloc analysis, and stable transformation of
and Sweet Clover souther: bloc analysis, and stable transformation of
and Sweet Clover souther: bloc analysis, and stable transformation of
and Sweet Clover souther: block and stable transformation of
the Alfalfa with antisense-lectin constructs.";

Bubmitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

Bubmitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

Bubmitted (
                                                                                                                                                                                                                                                                                                                                                              Medicago sativa (Alfalfa)

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae
eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDIINE=93000998; PubMed=1368792;
Estrada M.P., Hernandez L., Perez A., Rodriguez P., Serrano R.,
Rubiera R., Pedraza A., Padron G., Antuch W., de la Fuente J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "High level expression of streptokinase in Escherichia coli.";
Biotechnology 10:1138-1142(1992).
BMBL; 246536; AACG0418.1; -.
InterPro; IPRO4093; Staphylokinase.
Pfam; PF02821; Staphylokinase; 3.
SEQUENCE 414 AA; 47254 MW; F75BE5831B766904 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 10; Length 279; 100.0%; Pred. No. 54;
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                                                                                                                                                                                        Last sequence update)
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100.0%; Pred. No. 82;
ative 0; Mismatches
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                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23, Lectin precursor.
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Best Local Similarity 100.
Matches 6; Conservative
                                                          PRELIMINARY;
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Best Local Similarity 100.
Matches 6; Conservative
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279
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26 2
279 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Chief;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3879;
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Q53284;
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                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-16M / ATCC 23456 / Biotype 1;

STRAIN-20202109; PubMed=1175688;

MEDLINE=202020109; PubMed=1175688;

A DelVecchio V.G., Kapatral V., Fatkar R.J., Patra G., Mujer C., Los T.,

La Joblonski L., Larenn N., D'Souza M., Bernal A., Mazur M., Goltsman B.,

A Joblonski L., Larenn N., D'Souza M., Bernal A., Mazur M., Goltsman B.,

A Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

The genome sequence of the facultative intracellular pathogen

NT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

REMBL, ARGOSSO21, ARGISSB1.1;

REMBL, ARGOSSO21, ARGISSB1.1;

REMBL, ARGOSSO21, ARGISSB1.1;

REMBL, REMORDING: Low—mwt_PTPase.

REMBL, REMORDING: Low—mwt_PTPase.

REMBL, REMORDING: Low—mwt_PTPase.
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MEDLINE-22247741; PubMed=12271122;

PaulBen I.T., Seehadari R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
PaulBen I.T., Seehadari R., Durkin A.S., Kolonay J.F.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.
Riedmuller S., Tettelin H., Gill S.W., White O., Salzberg S.L.,
Hoover D.L., Lindlar D.E., Halling S.M., Boyle S.M., Fraser C.M.;
animal and plant pathogens and symbionts ";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                            Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
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Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. 29;
iive 0; Mismatches 0;
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les 6; Conservative
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Brucella melitensis.
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                                                                                                                                      NCBI_TaxID=29459;
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STRAIN=306 / ATCC 13302 / XV 101;
MEDILNE=22022145; Pubhed=12024217;
MEDILNE=22022145; Pubhed=12024217;
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Receptor protein-tyrosine kinase (Fragment).
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria, Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
NCBI_TaxID=6087;
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Xanthomoras axonopodis (pv. citri).
Bacteria; Proteobacteria; Ganthomonadales; Xanthomonadaces; Xanthomonadacese; Xanthomonadacese; Xanthomonadacese; Xanthomonadacese; Xanthomonadacese; Xanthomonadacese;
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STRAIN=UCI;
Chen R.L., Steele R.E.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U24116; AAA65223.1;
HSSP; P11362; 1FGK.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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nes 6; Conservative
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                                                                                                                                  157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 SVDVEY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVDVEY 6
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08PHD3
AC 08PHD3;
DT 01-0CT-7
DT 01-0CT-7
DE Acriflay
GN ACRF OR
COC MACRF OR
COC MACRF OR
COC NCBL TAI
RN (1)
RP SEQUENCI
RC MEDLINE:
RX MEDLINE:
RA ALVASE L
RA CAMAZOEI
RA CAM
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RAY CLEAR 11 12 PETERIA A.J. S. CHITHO L.L. CHITHO SHORE A. S. RETERIA A.J. S. RETERIA R.C.C., PETERO B. S. RETERIA A.J. S. RETERIA R.C.C., PETERO B. S. RETERIA B. S. CHITHO C. S. RETERIA R. S. RETERIA B. S. RETERIA S. RE
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100.0%; Score 30; DB 16; Length 1041;

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Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                          34 SIDVEY 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                      1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=601;
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                                                                                                                                                                                                                                                                                                                                                                                       Q9L5P9;
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016567
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                                    Gaps
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Dunaliellaceae, Dunaliella.
NCBI_TaxID=3046,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
DE Nicotinic acetylcyoline receptor Dalpha 4 subunit (Fragment)
3N NACR-ALPHA-808 OR NACALPHA-808 OR CG12414 OR CG17552.
C Drosophila melanogaster (Fruit fly)
C Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
C Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
K NCBL TaxID=7227;
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Pfam; PF00405; transferrin, 5.
PRINTS, PR00422; TRANSFERIN.
SMART; SM00094; TR FER; 1.
SEQUENCE 1274 AA; 136668 MW; 6C2EE9D914097699 CRC64;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Fisher M., Gokhman I., Pick U., Zamir A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U77059; AAB36531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         Created)
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                                 6; Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                           46 SVDVEY 51
                                                                                          1 SVDVEY 6
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SEQUENCE
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P93125;
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P93125
LD P9312
AC P931
AC P1
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409 RRA
100 RA
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                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                         Salmonella typhi.
Jebamid K27, and Plasmid pHCM1.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Salmonella.
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 Length 60;
                                  0; Indels
                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 15, Last sequence update)
Orf, hypothetical protein (Hypothetical 8.2 kDa protein)
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DCC7A8A73B746EAF CRC64;
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Last annotation update)
     'n
96.7%; Score 29; DB
83.3%; Pred. No. 18;
ive 1; Mismatches
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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BMBL, AL513383; CAD09627.1; -.
Hypochetical protein; Plasmid, SEQUENCE 74 AA; 8199 MW; DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                      PRELIMINARY;
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01-MAR.2002 (TEMBLrel. 20, Created)
01-MAR-2002 (TEMBLrel. 20, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annocation update)
Non-alpha nicotinic acetyloholine receptor subunit.
Aplysia californica (California sea hare).
Rukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda, Apogastropoda, Heterobranchia, Buthyneura, Opisthobranchia, Anaspidea, Aplysioidea, Aplysioidea, Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sadreyev R.I., Penchin Y.V., Meleshkevich E.A., Moroz L.L.;
"Non-alpha nicotinic acetylcholine receptor subunit from the
individual identified neurons of Aplysia californica.";
Submitted (Nov-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL, AF322876; AAL37250.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
AKBAI L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baččeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Wigglesworthia.
NCBI_TaxID=164609;
                                                                                                                                                96.7%; Score 29; DB 16; Length 215; larity 83.3%; Pred. No. 71; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%; Score 29; DB 16; Length 360; 83.3%; Pred. No. 1.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the endocellular obligate symbiont of
                                                                                      Complete protecme. SEQUENCE 215 AA; 24421 MW; C4334F6313CBFC15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 AA; 41359 MW; CA18CB13C1B8492B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              QBCWI5;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 AA
                      Pfam; PF00702; Hydrolage; 1.
PRINTS; PR00413; HADHALOGNASE.
TIGRFAMB; TIGR01509; HAD-SF-IA-v3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24654.1; -.
Complete proteome.
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  InterPro; IPR005834; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wigglesworthia brevipalpis.
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Best Local Similarity 83.55.
Them 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
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SIDVEY 30
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                                                                                                                                                                                                                                         1 SVDVEY 6
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HEME.
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Q8CWIS
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                                                                                                                        Milson R., Anscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copesy T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 824 / DSM 792 / VXM B-1787,
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.,
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acecoburylicum.";
J. Bacteriol. 183:4623-4638 (2001).
EMBL, AE007819; ARAR1166.1;
InterPro, IPR005833; HIgnase/hydrlase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF016658 1.
WormPep, 100047.4; CE07676.
InterPro; IPR002083; MATH.
Pfam; PF00917; MATH; 1.
SMART; SM0061; MATH; 1.
SEQUENCE 186 AA; 21527 MW; 9E216690AB0E1469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pauley A., Goela D., Ozersky P.;
"The sequence of C. elegans cosmid B0047.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Predicted phosphatase, HAD superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 5;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                    STRAIN-Bristol N2;
MEDLINE-94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pauley A., Goela D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 SIDVEY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Query Match

Matchea

097E84; **097E84**

RESULT 12

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Gaps

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us-09-919-703-1.open.rspt

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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                              crococcineae, Micrococcaceae, Arthrobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  772 SVDIEY 777
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                                                  NCBI_TaxID=1665;
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Q9FGN0
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Manteuffel R., Stoltenburg R., Kunze G.;
Manteuffel R., Stoltenburg R., Kunze G.;
Monteuffel R., Stoltenburg R., Kunze G.;
Monteuffel R., Stoltenburg R., Kunze G.;

Monteuffel R., Stoltenburg R., Kunze G.;

Veagat Arxula adeninivorans LS3.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ270833; CAB90817.1;

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR001117; Cu-oxidase.

Pfam; PF00394; Cu-oxidase; 3.

PROSITE, PS000099; MULTICOPPER OXIDASE1; 1.
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
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                    InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRIMTS; PR00252; NRIONCHĀNNEL.
TIGRRĀMS; TIGRO0680; LIC; 1.
PROSITE; PS00236; NEUROTR_ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                Query Match 96.7%; Score 29; DB 5; Length 547; Best Local Similarity 83.3%; Pred. No. 1.9e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.7%; Score 29; DB 3; Length 615; 83.3%; Pred, No. 2.2e+02; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                  547 AA; 62535 MW; 3D3F011D78605C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERRO-02-OXIDOREDUCTASE. 79200D42A28715E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Ferro-O2-oxidoreductase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9AGP8 PRELIMINARY; PRT; 830 AA. Q9AGP8; UJVN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) N.N-dimethylglycine oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
  InterPro; IPR006202; Neur_chan_LBD
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18 615 FE
615 AA; 69624 MW;
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es 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            155 SIDVEY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 SVDIEY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=37620
                                                                                                                                                                                                 Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=LS3;
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Q9P861
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09AGPB
1D 09AGPD
DT 01-JU
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DT 01-JU
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OSFGNO;
01-MAR-2001 (TERMELrel. 16, Created)
01-MAR-2001 (TERMELrel. 16, Last sequence update)
01-MAR-2001 (TERMELrel. 16, Last sequence update)
01-DEC-2001 (TERMELrel. 19, Last annotation update)
Similarity to unknown protein.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolophyta; eudicotyledons; core eudicots; Rosidae;
PUCBI_TAXID=3702;
SEQUENCE FROM N.A.
STRAIN=NRRL B-2979;
Meskys R., Harris R.J., Casaite V., Basran J., Scrutton N.S.;
Genetic organization of the genes involved in dimethylglycine and
sarcosine degradation in Arthrobacter spp.: implications for glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Kaneko T., Katoh T., Agamizu E., Sato S., Nakamura Y., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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OBIL36;

OBIL36;

OL-MAR-2003 (TrEMBLrel. 23, Created)
OL-MAR-2003 (TrEMBLrel. 23, Last sequence update)
OL-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
PR14 0413.
Butaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.7%; Score 29; DB 10; Length 836; Best Local Similarity 83.3%; Pred. No. 3e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    96.7%; Score 29; DB 2; Length 830;
83.3%; Pred. No. 3e+02;
ive 1; Mismatches 0; Indels
                                                                                                                     betaine catabolism.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF329477; AAK16482.1;
                                                                                                                                                                                            InterPro; IPRO06622; GCV T.
InterPro; IPR006076; IPR006076.
InterPro; IPR000205; NAD binding.
InterPro; IPR000594; ThiF_domain.
Pfam; PF01266; DAO; 1.
SEQUENCE 830 AA; 89984 MW; 13DE3C4B3DF325DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        836 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Q81L36
DD Q81L3.
AC Q81L3
DT 01-MA.
DT 01-MA.
DT HYDOL GN PF14
GN PF14
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Length 1154;

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Conservative
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les 5; Conservative
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                                                                                                                                                                               |||:||
117 SVDIEY 122
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          Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                             1 SVDVEY
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OBMMK4;
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                                                                                                                      Gardine M.J., 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911, 1911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FO9F7.3.
Caenorhabditis elegans.
Ebkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- ÇATALYTIC ACTIVITY: N NUCLECSIDE TRIPHOSPHATE = N DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!-SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
BEMEL; U00050; AAA50695.2;
WOTMPEP; F09F7.3; CE30663.
INTERPEO; PRO01572; RNA POL_BETA; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
MYPOCHPETICAL PROCESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 129.1 kDa protein (EC 2.7.7.6) (DNA-directed RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 862;
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83.3%; Pred. No. 3.1e+02;
Live 1; Mismatches 0; Indels
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EMBL; AE014823; AAN37026.1; -.

Hypothetical protein.

SEQUENCE 862 AA; 102256 MW; C0073FA8200E178C CRC64;
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Submitted (MAX-1994) to the EMBL/GenBank/DDBJ databases
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                                                                                              MEDLINE=22255705; PubMed=12368864;
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STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.5.
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[1]
SEQUENCE FROM N.A.
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Q27492;
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                                                               Glockher G., Bichinger L., Szafranski K., Pachebat J., Dear P., Glockher G., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A., Sequence and Analysis of Chromosome 2 of Dicryostellum."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caldicellulosiruptor sp. Rt69B.1.
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
Caldicellulosiruptor.
NCBI_TaxID=70295;
                                                                                                                                                                      Gaps
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-!- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL. HYDROLASES).
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Morris D.C., Gibbs M.D., Ford M., Thomas J., Bergquist P.L.;
"Family 10 and 11 xylanase genes from Caldicellulosiruptor spansing the strong of the spansing o
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R HSSP; P23360; 1K6A.

InterPro; 1PR0013105; CBM CenC.

R InterPro; IPR001119; SLH.

R Pfam; PF00313; Glyco_hydro_10.

R Pfam; PF00313; Glyco_hydro_10; 1.

R Pfam; PF00331; Glyco_hydro_10; 1.

R Pfam; PF00335; SLH; 3.

R RNATS; PR00134; GLHYDRLASE10.

SMART; SR00633; GLYCOSYL HYDROL F10; 1.

R PROSITE; PS00699; GLYCOSYL HYDROL F10; 1.

W Glycosidase; Hydrolase; Xylan degradation.

O SEQUENCE 1595 AA; 178404 MW; BC31B2363F30EF5B CRC64;
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83.3%; Pred. No. 6e+02;
iive 1; Mismatches 0; Indels
96.7%; Score 29; DB 5; Length 115
83.3%; Pred. No. 4.2e+02;
ive 1; Mismatches 0; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Family 10 xylanase (EC 3.2.1.8).
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01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MOST (TrEMBLRel. 23, Last annotation update)
Dictyostelium discoideum (Slime mold).
Eukaryott, Mycecozoa, Dictyosteliida, Dictyostelium.
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                                                                                                                                                                          Infect. Immun. 69:2083-2091(2001)
EMBL; AF078553; AAK28682.1; -.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
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Matches 4; Conservative
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Best Local Similarity
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23 SIDIEY 28
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SIDIEY 76
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NCBI_TaxID=10276;
   STRAIN=Oklahoma;
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Q8FU72
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Q8V3P9
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MEDLINE=21914557; PubMed=11916376;
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Mesyanzhinov V.V., Sykilinda N.N., Krylov V.N., Volckaert G.;
Bourkaltseva M.V., Sykilinda N.N., Krylov V.N., Volckaert G.;
"The genome of bactriophage phiKZ of Pseudomonas aeruginosa.";
J. Mol. Biol. 317:1-19(2002).
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Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Bourkaltseva M.V., Sykilinda N.N., Krylov V.V., Volckaert G.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF399011; AAL83091.1; --
InterPro, IPR001596; Pyrophosphatase.
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=169683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enrlichia canis.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
                                                                                96.7%; Score 29; DB 5; Length 2473; 83.3%; Pred. No. 9.5e+02; cive 1; Mismatches 0; Indels
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EMBL; AC117082; AAM34363.1; -. SEQUENCE 2473 AA; 274970 MW; 6395FD78E45A7945 CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 17.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                        146 AA
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MEDLINE=98371112; Pubmed=9705412;
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                                                                                                                  Local Similarity 83.3
nes 5, Conservative
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SVDIEY 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|:||
94 SIDIEY 99
                                                                                                                                                                                                      1 SVDVEY 6
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[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                 666
                                                                                      Query Match
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09ADW
AC 09ADW
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE HYPOT
OS BARTI
OX NCBI
RN NCBI
RN SEQUE
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RX MEDLI
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STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayaai Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.,
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=21624277; PubMed=11752168;
Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
MEDLINE=21153566; PubMed=11254561;
Mabshi N., Rikhihsa Y., Unver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer Membrane Protein Multigene Family in Ehrlichia canis and E.
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NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; Score 28; DB 16; Length 387; 66.7%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                          93.3%; Score 28; DB 2; Length 148; 66.7%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                               Hypothetical protein.
SEQUENCE 148 AA; 17570 MW; AF3545DF658F05BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 AA; 41402 MW; 45D83B7761CCB52F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 AA
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                                                                                                                                                                                                                                                                                                            2; Mismatches
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NON_TER 1 1
SEQUENCE 136 AA; 15535 MW; D6B9F39529DD5D3A CRC64;
       Created)
Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Protein kinase like-protein (Fragment)
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RMBL; S83367; AAB50855.1;
InterPro: 1P0000719; Prot. kinase.
Pfam; PF00069; pkinase; 1.
Probom; PD000001; Prot. kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
       01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                                                                                                                                Caenorhabditis elegans
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|:||
18 SIDIEY 23
                                                                                                            C08F11.14 protein.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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012377
              SO DE RELEASE DE LA DESENTA DE LA DELLA DE LA DELLA DE
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Science 282:2012-2018(1998).

- Science 282:2012-2018(1998).

- Socience 282:2012-2018(1998).

- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

R PMEL, Z50029, CA990341.2;

R MormPep, ZC5042, CC28383.

InterPro; IPR006201; Neur_chan.el.

InterPro; IPR006202; Neur_chan.el.

InterPro; IPR006202; Neur_chan.el.

R InterPro; IPR006202; Neur_chan.ell.

R Pfam; PF02931; Neur_chan.ell.

R Pfam; PF02931; Neur_chan.ell.

R Pfam; PF02932; Neur_chan.ell.

R Pf029333; Neur_chan.ell
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                     STRAIN=17077-99;
Afonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
Kutish G.F., Rook D.L.;
Submitted AUG-2001 to the EMBL/GenBank/DDBJ databases.
EMBL, AF410153; AAL69784.1;
InterProy IPR004970; Peptidase C57.
Pfam; PF03290; Peptidase C57: 1.
SEQUENCE 433 AA; 51052 MW; 2F9F7F0CE436A7D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.3%; Score 28; DB 5; Length 579; 66.7%; Pred. No. 3.5e+02; ive 2; Mismatches 0; Indels
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
"The genome of swinepox virus."; J. Virol. 76:783-790(2002).
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01-OCT-2001 (TrEMBLrel. 18,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 66.7
Matches 4; Conservative
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Matches 4; Conservative
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388 SIDIEY 393
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150 SIDIEY 155
                                                                                                        SEQUENCE FROM N.A.
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2C504.2.
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RESULT 26
023355
AC 023355
AC 02335
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DE 2C504
GN Caeno
OC Rhabd
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Q23355 Q23355;

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RESULT 27 Q9U3Q5 ID Q9U3Q5 AC Q9U3Q5;

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MEDLINE=97128994; PubMed=8973534;
MEDLINE=97128994; PubMed=8973534;
Jang H.K., Ono M., Kato Y., Tohya Y., Niikura M., Mikami T.;
"Identification of a potential Marek's disease virus serotype 2
glycoprotein D gene with homology to herpes simplex virus glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Science 282:2012-2016(1998).
Rembl; 28316; CAB62784.1; -.
HSSP; O53752; Irfol.
MormPep; CO8FI1.14; CE23529.
RINTERPO; IPRO06254; ISCOIT lyase.
InterPro; IPRO06252; Malate synthas.
InterPro; IPRO01865; Malate synthase.
RinterPro; IPRO01465; Malate synthase.
Rem; PF01274; Malate synthase.
ProDom; PF001867; ISCOIT lyase_ph; 1.
RIGREAMS; TIGRO1346; iscoit lyase, 1.
RESULT RESULT RATE LYASE; 1.
SEQUENCE 907 AA; 101848 MW; AAF64B820B82D1B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.3%; Score 28; DB 5; Length 907; 66.7%; Pred. No. 5.7e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                         Matthews L.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
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Query Match
Beet Local Similarity 83.3%;
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Q8X2B1;
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ID Q8
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SYNRARAS
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Rhabditidae; Peloderinae; Caenorhabditis.
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Spodoptera frugiperda ascovirus 1.
Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
                90.0%; Score 27; DB 12; Length 136; 83.3%; Pred. No. 1.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%; Score 27; DB 5; Length 180; 83.3%; Pred. No. 1.8e+02; ive 1; Mismatches 0; Indels
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EMBL; U28971; AAA68377.1;
WormPep; B0244.9; CE01756.
InterPro; IRR01065; Ribosomal S2.
PROSITE: PS00962; RIBOSOMAL_S2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid B0244."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. - SEQUENCE 180 Aa; 20592 MW; 9B41BA9212622FD4 CRC64;
                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 20.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBJJY6;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                Query Match
Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.; "Direct Submission.";
                                                                                                                                                 92 SMDVEY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                          1 SVDVEY 6
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STRAIN=a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Favello A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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000966
AC 000966
AC 00096
DT 01-NO
DT 
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expansin-like protein (Fragment).
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935, PubMed=11206551,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Enterobacteriales,
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U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last amontation update)
Putative tail fiber protein encoded within prophage CP-933V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.0%; Score 27; DB 10; Length 213; 83.3%; Pred. No. 2.1e+02; ive 1; Mismatches 0; Indels
Stasiak K., Renault S., Demattei M.V., Bigot Y., Federici "Evolution of Ascoviruses from Iridoviruses"; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ312699, CAC84464.1; -. InterPro; IPR002624; dNK.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.0%; Score 27; DB 12; Length 21 Best Local Similarity 83.3%; Pred. No. 2.1e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 210 AA; 24522 MW; 9B28484AF10C6B79 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL; AY100693; AAM52409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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MEDLINE=22315554; PubMed=12428004;
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Enterobacteriaceae; Escherichia
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MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
"Oryza sativa chromosome 10 BAC OSJNBb0015111 genomic sequence.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
EMBL; AC051633; AAG13596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea, Buryarchaeota, Thermoplasmata, Thermoplasmatales,
Thermoplasmataceae, Thermoplasma.
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                                                                                                                                                         InterPro; IRR007112; Expan_endogl.
InterPro; IRR007113; Expan_Lol_pl.
InterPro; IRR007113; Expan_Lol_pl.
InterPro; IRR007117; Expan_Lol_pl.
Proists; PR01225; ExPaNSNFAMLY.
PRODITS; PR002179; Expan Lol_pl C; 1.
PROSITE; PS00842; ExPANSIN_EGB5; 1.
PROSITE; PS0842; ExPANSIN_EG45; 1.
SEQUENCE 275 AA; 29301 MW; E088C7DF0596AIC7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Ta0490.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 10;
Pred. No. 2.8e+02;
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EMBL; AL445064; CAC11632.1; ...
InterPro; IPR002235; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Expansin-like protein 1.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                     Gramene; Q9FWF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DSM 1728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY
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091GS6
001GS AC 091GS
DT 01-0C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. Nipponbare,
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.B.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
            Welch R.A., Blattner F.R., Gacome esquence of enterchaemorrhagic Escherichia coli O157:H7."; Mature 409:529-533(2001).
EMBL, AE005440; AAG57198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Elihartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                  Length 271;
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                                                                                                                                                                                                                            90.0%; Score 27; DB 16; Length 27
83.3%; Pred. No. 2.7e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                  Complete proteome.
SEQUENCE 271 AA; 27706 MW; CE4D5CB197BB3B1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3.
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OSJNBB0015111.10.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                               52 SMDVEY 57
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                                                                                                                                                                                                                                                                                                                                                        1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=83334;
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Q8X298;
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08829
AC 08829
AC 08829
AC 01-MAD 01-MAD 01-MAD 01-MAD 01-MAD 01-MAD 01-MAD 01-MAD 02 Bacte 00 C Bac
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O9FWF9
AC Q9FWF
AC Q9FWF
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SEQUENCE FROM N.A.

STRAIN-CJ0149;

MEDLINE-21107697; PubMed=11158621;

MEDLINE-21107697; PubMed=11158621;

MAND F.;

MAND F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.0%; Score 27; DB 12; Length 302; Best Local Similarity 83.3%; Pred. No. 3.1e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 27; DB 17; Length 307; 83.3%; Pred. No. 3.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrobaculum aerophilum,
Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 AA; 33783 MW; 07134831A775D358 CRC64;
                                                                                                                                                                                                                                                Viruses, dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=106331;
Q993F5 PRELIMINARY; PRT; 302 AA. Q993F5; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update) ORF54.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acrophilum.",
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
InterPro; IPR009514; AALG4915.1; ...
InterPro; IPR006139; 2-Hacid_DH..
Fam; PF02886; 2-Hacid_DH..
Pros. IE; PS00670; D.Z. HyDROXYACID_DH.2; I.PROSITE; PS00670; D.Z. HYDROXYACID_DH.3; I.Complete proteome.
SRQUENCE 307 AA; 33783 MW; 07134831A775D358 CR
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
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                                                                                                                                                                                                                                 Callitrichine herpesvirus 3.
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Best Local Similarity 83.5-
5; Conservative
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221 AVDVEY 226
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76 NVDVEY 81
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           ID DOT THE REAL PROPERTY OF TH
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"Rice Genomic Sequence.";
"Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 27; DB 10; Length 279; 83.3%; Pred. No. 2.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%; Score 27; DB 10; Length 289; 83.3%; Pred. No. 2.9e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                               "Expression of expansin-like genes in rice internodes."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. -- I- SINILARITY: BELONGS TO THE EXPANSIN FAMILY. EMBL, AXO39902, AAK84681.1; -- Gramene; O9LGS6; --
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InterPro; IPR07112; Expan_endogl.
InterPro; IPR071112; Expan_endogl.
InterPro; IPR071118; Expan_Lol_pi.
InterPro; IPR07117; Expan_Lol_pi.
Pfam, PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
PROSITE; PS50843; ExpanSIN_EG45; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
SEQUENCE 289 AA, 31238 WW; 5EF4D782ATEF7322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   InterPro; PR007112; Expan endogl.
InterPro; IPR007113; Expan_Lol_Dl.
InterPro; IPR007117; Expan_Lol_Dl.
InterPro; IPR007117; Expan_Lol_Dl.
Pfam; PF0137; Pollen allergen; 1.
Prolom; PF0127; Expan_SNPAMLY.
Procom; PD02179; Expan_Lol_Dl_C; 1.
PR0SITE; PS50842; ExpanSIN_CED; 1.
PR0SITE; PS50842; ExpanSIN_CED; 1.
SEQUENCE 279 AA; 30038 MW; FD9B86A5A6A9BA2B CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative pollen allergen.
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               Ehrhartoideae, Oryzeae, Oryza.
NCBI_TaxID=4530;
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Ouest Local Similarity 83.33,
Best Local Si Conservative
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Best Local Similarity 83.3,
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146 AVDVEY 151
                                                                                                                          SEQUENCE FROM N.A.
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RESULT 37
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AC 08150
DT 01-0C
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RESULT 38 Q993FS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane lipoprotein.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.5.
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LIPL41.
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Best Local Similarity
Matches 5; Conserv
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23 TVDVEY 28
                                                                                                                                                                                                                                                      Complete proteome.
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                                                                                                      Hopwood D.A.;
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P71435;
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                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:655-573(2002).
EMEL, AKO89832; BAC39034.1; -.
SEQUENCE 320 AA; 34522 MW; 91DC3FBF778631C8 CRC64;
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAIN=A3[0.7] / M.45;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=2199640. PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%; Score 27; DB 11; Length 320; 83.3%; Pred. No. 3.3e+02; ive 1; Mismatches 0; Indels
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown S.P., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ceroid-lipofuscinosis
Mus musculus (Mouse).
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STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
MEDLINE=22354683; PubMed=12466851;
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MEDLINE=97000351; PubMed=8843436;
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Best Local Similarity 83.3
Lac 5, Conservative
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                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium,
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SLDVEY 36
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                                                                                                        01-MAR-2003
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208BNF3
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Q9L074
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MEDLINE=96239055; PubMed=8675344;
Shang E.S., Summers T.A., Haake D.A.;
"Molecular cloning and sequence analysis of the gene encoding LipL41,
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Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
VCBI_TaxID=173;
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=29507;
                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417.141-147(2002).
EMBL; AL939113: CAB87377.1; -.
InterPro; IPR002491; Peripla BP.
Pfam; PF01497; Peripla_BP_2; 1.
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83.3%; Pred. No. 3.6e+02;
tive 1; Mismatches 0; Indels
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83.3%; Pred. No. 3.6e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            349 AA; 36642 MW; 2E3B2A72B6BF780A CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morris K.K.;
Thesis (1995), University of California, Davis.
EMBL; U31426; AAB09404.1; -.
Lipoprotein.
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SEQUENCE FROM N.A.
STRAINSATC2 2586;
MEDLINE=21886394; PubMed=11889109;
MEDLINE=21886394; PubMed=11889109;
MEDLINE=21886394; PubMed=11889109;
Mathacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 2586.";
J. Bacteriol. 184:2005-2018(2002).
EMBL. AEO18883. AAL93958.1; -.
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    Fusobacterium nucleatum strains and a model for the topology of the
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Bacteria; fusobacteria; fusobacterales; fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                          90.0%; Score 27; DB 2; Length 368 83.3%; Pred. No. 3.8e+02; Ative 1; Mismatches 0; Indels
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
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                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 368 AA; 42373 MW; 131624D9EB017626 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Major outer membrane protein.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Porin precursor.
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83.3%; Pred. No. 3.8e+02;
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                                                              proteins.";
Mol. Gen. Genet. 244:104-110(1994).
EMBL; X72582; CAAS1172.1; -.
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STRAIN-ATCC 10953;
MEDLINE-94316187; Pubmed-8041356;
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Best Local Similarity 83.34;
Best Local Similarity 83.34;
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Best Local Similarity 83.3
Matches 5; Conservative
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59 SVDVQY 64
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NCBI_TaxID=76856;
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SIGNAL
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Q47905;
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MEDLINE=94010332; PubNed=8406032;
MEDLINE=94010332; PubNed=8406032;
Bolstad A.I., Jensen H.B.;
"Complete sequence of only, the structural gene encoding the 40-kDa outer membrane protein of Fusobacterium nucleatum strain Fev1.";
Gene 132:107-112(1993).
Signal.
a surface-exposed lipoprotein of pathogenic Leptospira species.";
Infect, Immun. 64:2322-2330(1996).
EMBL; L46794; AAB06799.1; -.
InterPro; IPR001440; TPR.
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STRAIN=ATCC 25586;
MEDLINE=94316187; PubMed=8041356;
Boletad A.I., Tommassen J., Jensen H.B.;
"Sequence variability of the 40-kDa outer membrane proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 27; DB 2; Length 368; 83.3%; Pred. No. 3.8e+02; ive 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae; Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIĞNAL 1 20 POTENTIAL.
CHAIN 21 368 OUTER MEMBRANE PROTEIN (40K).
SEQUENCE 368 AA; 41918 MW; 13E15C1E2E3DEE82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 27; DB 2; Length 355
83.3%; Pred. No. 3.6e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                 1 19 POTENTIAL.
20 355 POTENTIAL.
355 AA; 38910 MW; 89D2EA08D271DC78 CRC64;
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047904;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein (40K) precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
Porin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 AA
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Best Local Similarity 83.3
Matches 5, Conservative
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Matches 5; Conservative
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23 TVDVEY 28
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SEQUENCE
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Q47904
ID Q47904
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AC Q47900
DT 01-NC
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1047903
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Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner P.R.;

T "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";

EMBL; AE005290; AAG55515.1; -.

R InterPro; IPRO00087; Collagen.

R Pfan; PF01391; Collagen; 2.

Complete proteome.

W Complete proteome.

SEQUENCE 375 AA; 37493 MW; 6BG3CF5F93757C62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                      Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
VCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bscherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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STRAIN=56601 / Serogroup Icterchaemorrhagiae / Serovar lai,
                                                                                                                                                                                                                                                                                                                                                                                              Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.0%; Score 27; DB 16; Length 375; Best Local Similarity 83.3%; Pred. No. 3.9e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.0%; Score 27; DB 16; Length 37 Best Local Similarity 83.3%; Pred. No. 3.9e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE011248; AAN47815.1;
Lipoprotein; Complete proteome.
SEQUENCE 374 AA; 41070 MW; 3A3F9EB94BFDCIAO CRC64;
                                                                                                  PRT;
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                                                                      PRELIMINARY;
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                                                                Q8F8E1
Q8F8E1;
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                                   RESULT 49
Q8F8E1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC;
MEDLINE=96179239; PubMed=8596666;
Bolerd A.I., Hogh B.T., Jensen H.B.;
"Molecular characterization of a 40-kDa outer membrane protein, FomA, of Fusobacterium periodonticum and comparison with Fusobacterium nucleatum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oral Microbiol. Immunol. 10:257-264(1995).
EMBL. X82023, CAAS747.1; -. MAJOR OUTER MEMBRANE 40KDA PROTEIN FOMA.
21 A3.72 A4.42265 WW, 5DFC806A50D48F56 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Bolstad A.I., Tommassen J., Jensen H.B.; "Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nucleatum strains and a model for the topology of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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90.0%; Score 27; DB 2; Length 372;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.0%; Score 27; DB 2; Length 370; 83.3%; Pred. No. 3.8e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusobacterium periodonticum.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                        Bolstad A.I.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 10953;
Jensen H.B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                      Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL 1 20 POTENTIAL.
CHAIN 21 370 PORIN.
SEQUENCE 370 AA, 42241 MW, 781611E6F206012F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2001 (TrEMBLrel. 19, Last annotation update)
Major outer membrane 40KDa protein FomA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 372 AA
                                                      proteins.";
Mol. Gen. Genet. 244:104-110(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X72583; CAA51173.2; -.
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Matches 5, Conservative
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                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 10953;
Bolstad A.I.;
                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 10953;
Bolstad A.I.;
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59 SVDVQY 64
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Search completed: January 20, 2004, 13:57:40 Job time : 39 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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January 20, 2004, 13:56:22 ; Search time 24 Seconds (without alignments) 18.415 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-919-703-1 30 1 SVDVEY 6 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

354356 segs, 73659510 residues Searched:

354356 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database :

Pending Patents AA New:*

1: /cgn2 6/ptodata/1/paa/PCT NEW COMB.pep:*

2: /cgn2-6/ptodata/1/paa/USO6 NEW COMB.pep:*

4: /cgn2 6/ptodata/1/paa/USO7 NEW COMB.pep:*

5: /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*

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6: /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*

7: /cgn2-6/ptodata/1/paa/USO8 NEW COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ٠ | | | | |
|---------------|-------|----------------|-----------------------|-----|------------------|-------------------|
| Result No. | Score | Query Match | Query Match Length | DB | ΩΙ | Description |
| | 30 | 100.0 | 440 | 1 9 | -415-182A-8 | 1 00 |
| 7 | 29 | 96.7 | 520 | ഹ | -09-614-1 | equence 2569 |
| m | 29 | 96.7 | 615 | 9 | -679-063-26 | e 268 |
| 4 | 29 | 9 | 1190 | Ŋ | -09-614-1 | equence 3243, A |
| Ŋ | 27 | 0 | 17 | ø | US-10-474-601-11 | 11, |
| 9 | 27 | 0 | w | 9 | -10-425-114A-59 | equence 595 |
| 7 | 27 | 0 | - | Ŋ | | e 2505 |
| æ | 27 | 0 | ₩. | 7 | -60-483-917 | equence 62, |
| on | 27 | 0 | 563 | 7 | -60-483-917-6 | Sequence 60, Appl |
| 10 | 27 | 0 | IO. | 7 | -60-482-992-1 | equence 14, |
| 11 | 26 | Θ | 77 | 9 | -10-425-1 | 5466 |
| 12 | 26 | w | 10 | 9 | .0-679-063-193 | 1932, |
| 13 | 26 | ø | 10 | 9 | -10-679-063-2 | equence 25025, |
| 14 | 26 | v | tn. | ø | 0-679-063-128 | 1285, |
| 15 | 56 | ø | M | 9 | -10-679-063-258 | 25896, |
| 16 | 26 | ø | 9 | 9 | 10-679-0 | 15897, |
| 17 | 26 | 9 | ~ | 9 | 5-18 | 3474, A |
| 18 | 26 | 9 | 0 | Н | r-US03-40618-72 | 7251, |
| 19 | 26 | ø | 201 | 9 | -10-741-849-7 | equence 7 |
| 20 | 26 | ø | ч | ۲ | 0-495-114-157 | 157 |
| 21 | 26 | ė | 4 | 9 | -10-389-647-69 | equence 692 |
| 22 | 26 | ė | α | 9 | -10-701-283-4 | e 43, |
| 23 | 56 | 86.7 | œ | 9 | -10-701-283 | 4 |
| 24 | 56 | Ġ | α | 9 | -283-1 | 12 |
| 25 | 56 | ů, | 303 | 2 | -09-614-150A- | e 361 |
| 26 | 26 | 86.7 | Н | 2 | -09-897-516A-661 | e 661 |
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| 60 | 094 | 0318 | 892, | 698, | 83, | 47, | 786, | 687 | 191, | 056, | 707, | 6, 4 | ∢. | 8810 | 81, | 68, | Æ. | 67, | 42 | | 857 | 8237 | 72, | 4656 | 4273 | 848, | 01, | 9431 | 378 | 5585 | 285 | ò | ď | ∢. | 4434 | 1168 | 847 | 7455 | 690, | 742 | 5236 | ∢. | 968 | 361 | ο, | 4 | 437 | , 0, |
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| Sequence | Sequence | a) | Sequence | a) | Sequence | eg G | Ð | еđ | ø | Seguence | Sequence | Sequence | Sequence | Sequence | egu | еq | Seguence | ednenc | edneuc | ednenc | Sequence | Seguence | Sednence | Sequence | Sequence | eda | Sequence | equ | Sequence | egr | Sequence | Sequence | Sequence | egn | egu | e d | Sequence | Sequence | Sequence | egr | Sequence | Sequence | Seguence | eg. | a) | Sequence | Sequence | Sequence |
| S-10-425-114A-400 | US-10-425-114A-64094 | S-10-739-930-1031 | S-10-415-182A-9 | S-10-415-182A-269 | S-10-473- | 8-60-479-962-44 | 8-10-739-930-5786 | 8-10-679-063-166 | S-10-679-063-21 | S-10-472-928-305 | 5-10-679-063-270 | 8-10-451-168-5 | 8-10-451-168-57 | S-09-614-150A-1 | S-09-614-150A-398 | 8-60-495-589-16 | S-10-418-861B-4 | 8-10-475-292-167 | S-09-581-286A-44 | S-09-581-286A-316 | S-09-614-150A-16 | S-09-614-150A-182 | S-10-472-928-972 | S-10-425-114A-54 | 8-10-679-063-2427 | S-10-679-063-984 | 8-10-679-063-9601 | 8-10-679-06 | 8-10-679-063-1937 | S-10-425-114A-455 | S-10-425-114A-3728 | 8-10-472-260-160 | S-10-275-026A-1 | S-10-275-026A-44 | S-10-425-114A-4443 | S-10-425-114A-511 | S-10-425-114A-6384 | 8-10-679-063-1745 | S-09-897-516A-6690 | S-10-425-114A-537 | S-09-614-150A-2523 | CT-US03-30770-1 | S-10-425-114A-6 | S-10-425-114A-7236 | 8-10-679-063-85 | -679-063-3844 | S-09-614-150A-40 | -10-415-182A-654 |
| 9 | ø | 9 | 9 | 9 | ø | 7 | 9 | 9 | 9 | ø | 9 | 9 | 9 | ŝ | Ś | 7 | 9 | 9 | ស | 'n | S | ហ | ø | 9 | 9 | ٥ | 9 | 9 | φ | 9 | 9 | 9 | 9 | 9 | 9 | 9 | ø | φ | Ŋ | 9 | ഹ | Н | 9 | 9 | 9 | 9 | S | 9 |
| m | マ | ø | 0 | N | 428 | 4 | 2 | 9 | 3 | 7 | σ | 0 | 0 | Н | c | 7 | 7 | œ | σ | 83 | œ | 13 | 20 | ~ | ß | S | ŝ | 9 | 9 | 4 | 4 | 9 | 7 | 7 | œ | σ | N | S | m | 7 | 0 | Η. | N | N | C4 | 424 | £ | 466 |
| 86.7 | 86.7 | 86.7 | 86.7 | 9 | ġ. | ġ. | 9 | ė | è. | 9 | è. | 9 | ė. | 9 | ė. | è. | è. | é. | ė. | 9 | 9 | 9 | 'n. | ë. | m. | س | ω. | ش | m. | e. | ო | | m. | е Н | ٠ ش | щ. | 'n | ო | ٠. ش | ci | ٠. ش | m. | ë | ო | ë | 83.3 | ë | m. |
| 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 56 | 26 | 26 | 26 | 56 | 26 | 56 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | . 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 |
| 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 4. | 20 | 51 | 52 | 53 | 54 | 52 | 99 | 57 | 28 | 59 | 9 | 61 | 62 | 63 | 64 | 65 | 99 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 |

ALIGNMENTS

RESULT 1
US-10-415-182A-8298
i Sequence 8298, Application US/10415182A
i GENERAL INFORMATION;
i APPLICANT: Telford, John
i TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
TITLE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/415,182A
CURRENT FILING DATE: 2000-12-09
i PRIOR PAPLICATION NUMBER: GB-0026333.5
PRIOR PAPLICATION NUMBER: GB-002672.6
j PRIOR APPLICATION NUMBER: GB-0105640.7
j PRIOR APPLICATION NUMBER: GB-0105640.7
j PRIOR APPLICATION NUMBER: GB-105640.7
j PRIOR FILING DATE: 2001-03-07
j NUMBER OF SEQ ID NOS: 12024
j SEQ ID NO 8228
j LENGTH: 440

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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Friedrich, Thomas
APPLICANT: Zimmerman, Norbert
APPLICANT: Zimmerman, Norbert
APPLICANT: Sturmer, Rainer.
TITLE OF INVENTION: Reaction of (di)amines in the presence
TITLE OF INVENTION: of a lysin oxidase and of a reducing agent
FILE REFERENCE: BGI-156US
CURRENT APPLICATION NUMBER: US/10/474,601
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: PCT/EP02/03873
PRIOR PILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.7%; Score 29; DB 5; Length 1190; 83.3%; Pred. No. 1.5e+03; ive 1; Mismatches 0; Indel8
                                                                                      Score 29, DB 6; Length 615;
Pred. No. 1.2e+03;
1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/614,150A CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 06/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/173,93
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/15,637
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SEQ TWARRE: FASISED FOR WINDOWN VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-614-150A-3243; Sequence 3243; Application US/09614150A; GENERAL INFORMATION:
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; ORGANISM: Arxula adeninivorans US-10-679-063-26860
                                                                                            96.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83...
7.20 St. Conservative
                                                                                            Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                      311 SVDIBY 316
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                                                                                                                                                                                                                           1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: et al.

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRANT FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR APPLICATION NUMBER: 60/191,637
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
ITILE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15,52054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 26860
LENGTH: 615
TYPE: PRT
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                                                                                                                          100.0%; Score 30; DB 6; Length 440; 100.0%; Pred. No. 8e+02; ive 0; Mismatches 0; Indels
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25695, Application US/09614150A GENERAL INFORMATION: APPLICANT: Venter, J. Craig
                                 ; ORGANISM: Streptococcus pyogenes US-10-415-182A-8298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.7%;
                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                 183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 SIDVEY 187
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US-09-614-150A-25695
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US-10-679-063-26860
   TYPE: PRT
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US-60-483-917-60

Sequence 60, Application US/60483917

GENERAL INFORMATION:

APPLICANT: Gan, Li

APPLICANT: Chin, Daniel J

TILE OF INVENTION: WIGGER ASSOCIATED WITH NEURODEGENERATIVE DISORDERS

TILE REFERENCE: 00208-0013-P2US00

CURRENT APPLICATION NUMBER: US/60/483,917

CURRENT PILING DATE: 2003-06-30

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin version 3.2

SEQ ID NO 60

LENGTH: 563

MANDE. ADM.
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APPLICANT: Shivak, David
APPLICANT: Shivak, David
APPLICANT: Shivak, David
APPLICANT: von Schack, David
APPLICANT: von Schack, David
APPLICANT: Gonzalez-Zulueter, Mirella
APPLICANT: Gonzalez-Zulueter, Mirella
APPLICANT: Gonzalez-Zulueter, Mirella
TITLE OF INVENTION: NUCLEIC ACIDS ASSOCIATED WITH NEURODEGENERATIVE DISORDERS
FILE REFERENCE: 00208.0013. PZ0S00
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.2
SEQ ID NO 62
LIBRORIT: 562
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                                                                                                                                                                                                                                                                                               Length 515;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                            90.0%; Score 27; DB 5; I
83.3%; Pred. No. 2.1e+03;
ive 1; Mismatches 0;
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25556
LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 62, Application US/60483917; GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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; ORGANISM: Rattus norvegicus
US-60-483-917-60
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 5, Conservative
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CRGANISM: Mus musculus
US-60-483-917-62
                                                                                                                                                                                        TYPE: PRT; ORGANISM: DROSOPHILA
US-09-614-150A-25056
                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 SVDMEY 456
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Cool, Yihua
APPLICANT: Cool, Yingu
APPLICANT: Tabaska, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59564
LENGTH: 268
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT PILING DATE: 1090-10-19
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PELING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-28
PRIOR PELING DATE: 1999-11-128
PRIOR PELING DATE: 1999-11-128
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/175,693
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                                                                                                                                                          90.0%; Score 27; DB 6; Length 17; 83.3%; Pred. No. 6.3e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB3587-216-D2_FLI.pep
US-10-425-114A-59564
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 59564, Application US/10425114A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-614-150A-25056
; Sequence 25056, Application US/09614150A
; GENERAL INFORMATION:
                                                                                                                                                                                        Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.3
Matches 5, Conservative
                             LENGTH: 17
TYPE: PRT
CRGANISM: Pichia pastoris
US-10-474-601-11
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1 NVDVEY 6
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ORGANISM: Zea mays
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US-10-425-114A-59564
          SEQ ID NO 11
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Sequence 25025, Application US/10679063

Sequence 25025, Application US/10679063

GENERAL INFORMATION: Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(2204)B

CURRENT FILING DATE: 2003-10-02

PRIOR PLICATION NUMBER: 60/415,758

PRIOR PLICATION NUMBER: 60/415,758

PRIOR PLICATION NUMBER: 60/415,758

FRIOR PLICATION DATE: 2002-10-02

NUMBER OF SEQ ID NOS: 27373

SEQ ID NO 25025

LEMCTH: 160

LEMCTH: 160

CENTRAL OF SEQ ID NOS: 27373

CORGANISM: Glycine max

US-10-679-063-25025
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TITLE OF INVENTION: TRANGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 30-15 (52054)B
CURRENT APPLICATION NUMBER: 02010/02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 1285
LENGTH: 164
TYPE: PRI
ORGANISM: Glycine max
            Sequence 1933, Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TITLE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NYBER: US/10/679,063
CURRENT APPLICATION NUMBER: 00/10/02
PRIOR FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 1932
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

86.7%; Score 26; DB 6; Length 158;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.8e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure

LOCATION: (1)..(158)

COTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-1932
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Best Local Similarity 83.3%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Glycine max
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     US-10-679-063-1932
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Abou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: ADABLICANT: ADABLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao, Yongwein;
ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILER REFERENCE: 30-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54666
LENGTH: 140
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Sequence 14, Application US/60482992

Sequence 14, Application US/60482992

Sequence 14, Application US/60482992

Sequence 14, Application US/60482992

APPLICANT: Li, Weihua

APPLICANT: Reed, Danielle

APPLICANT: Bachmanov, Alexander

CURRENT: Brand, Joseph

TITLE OF INVENTION: Taste Receptor Of The TIR Family From Domestic Cat

CURRENT APPLICATION NUMBER: US/60/482,992

CURRENT FILING DATE: 2003-06-27

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.2

SEQ ID NO 14

LENGTH: 858
                                                        Gaps
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  90.0%; Score 27; DB 7; Length 563; 83.3%; Pred. No. 2.1e+03; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 7; Length 858
Pred. No. 2.5e+03;
1; Mismatches 0; Indels
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US-10-425-114A-54666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%;
Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Rattus rattus
US-60-482-992-14
                                                                                                                                  |:||||
274 SLDVEY 279
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Best Local Similarity
Matches 5; Conserv
                                                                                                      1 SVDVEY 6
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ORGANISM: Zea mays
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US-10-425-114A-54666
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CURRENT APPLICATION NUMBER: US/10/415,182A
CURRENT PILING DATE: 2003-12-09
PRIOR PELLING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: GB-002872.6
PRIOR APPLICATION NUMBER: GB-005640.7
PRIOR APPLICATION NUMBER: GB-005640.7
PRIOR APPLICATION NUMBER: GB-005640.7
PRIOR FILING DATE: 2001-03-07
NUMBER: SEQ ID NOS: 12024
SEQ ID NO 3474
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GENERAL INPORMATION:
APPLICANT: Roemer, Terry
APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT CANDIDA Albicans PCT-US03-40618-7251
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-741-849-7251
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GENERAL INFORMATION:
TEDESTAL INFORMATION:
TITLE ENGERENCE: 38-15(2054)B
CURRENT PELICANT: 81-15(2054)B
CURRENT PELICANTES. 2003-10-02
CURRENT PELICATION NUMBER: US/10/679,063
CURRENT PELICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
LENGTH: 164
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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TILE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 15897
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                                                                                                               86.7%; Score 26; DB 6; Length 164; 83.3%; Pred. No. 1.9e+03; ive 0; Mismatches 1; Indels
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Pred. No. 1.9e+03;
0; Mismatches 1; Indels
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(164)
; OTH: INFORMATION: unsure at all Xaa locations
US-10-679-063-1285
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; Sequence 3474, Application US/10415182A
; GENERAL INFORMATION:
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US-10-679-063-15897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.78;
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US-10-679-063-25896
                                                                                                                 Query Match 86.7
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-679-063-25896
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US-10-679-063-15897
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APPLICANT: Blitra Pharmaceuticals, Inc.
APPLICANT: Elitra Pharmaceuticals, Inc.
APPLICANT: Elitra Canada Limited
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
CURRENT APPLICATION NUMBER: PCT/US03/40618
CURRENT PLING DATE: 2003-12-19
FRIOR FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PATENTION NUMBER: Us 60/434,832
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PATENTION NUMBER: Use 60/434,832
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PATENTION NUMBER: Use 60/434,832
LENGRANT: LENGRANT: LOS: 8000
SOFTWARE: PATENTION NUMBER: Use 60/434,832
LENGRANT: LOS: 8000
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
TITLE OF INVENTION: Use
FILE REPERENCE: 10182-023-999
CURRENT APPLICATION NUMBER: US/10/741,849
PRIOR APPLICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2003-12-19
APPLICANT: Telford, John
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A &
FILE REFERENCE:
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215 SADVBY 220

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NUMBER OF SEQ ID NOS: 8000

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APPLICANT: Spaceria Aceven A APPLICANT: Shamets, Steven A APPLICANT: Shimkets, Richard A. APPLICANT: Shimkets, Richard A. APPLICANT: Shimkets, Richard A. APPLICANT: Shimkets, Richard A. APPLICANT: Spaceria Padigaru APPLICANT: Spycek, Kimberly A. TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE APPERENCE: 1596-620 CIP CURRENT APPLICATION NUMBER: US/09/737,149
PRIOR APPLICATION NUMBER: US/09/737,149
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 1999-12-27
PRIOR PAPLICATION NUMBER: 60/173,165
PRIOR PLING DATE: 1999-12-27
PRIOR PLING DATE: 1999-12-27
PRIOR PLING DATE: 1999-12-29
PRIOR PLING DATE: 2000-01-04
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APPLICANT: Special, Steven K
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Muralidhara, Padigaru
APPLICANT: Spytek, Kimberly A.
CURRENT APPLICATION NUMBER: US/10/701,283
PRIOR APPLICATION NUMBER: US/09/737,149
PRIOR APPLICATION NUMBER: 60/170,564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (1)...(282)
OTHER INFORMATION: Where X is a residue at which the query and
OTHER INFORMATION: Subject seugnces are not identical.
US-10-701-283-43
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus Sequence
                                                                                              RESULT 22
US-10-701-283-43
i Sequence 43, Application US/10701283
; GENERAL INFORMATION:
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                                                                                                                                                                                                          APPLICANT: Spaderna, Steven K
APPLICANT: Quinn, Kerry E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66...
4; Conservative
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2 AVDIEY 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT APPLICATION NUMBER: US/60/495,114
SOFTWARE: FALUE DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FALUE OF Mindows Version 4.0
SEQ ID NO 1576
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Pred. No. 2e+03;
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GENERAL INFORMATION:
APPLICANT: GERENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTRCH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR APPLICATION NUMBER: 60/153022
PRIOR FILING DATE: 1999-09-01
MUMBER OF SEQ ID NOS: 710
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 692
LUMBER OF SEQ ID NOS: 710
SEQ ID NO 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 7; Length 212;
83.3%; Pred. No. 2e+03;
tive 1; Mismatches 0; Indels
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Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                             86.7%; Scc...
100.0%; Pred. No. ...
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US-10-389-647-692
SOFTWARE: Parentin Version 3.2

SEQ 1D NO 7251

LENGTH: 201

TYPE: PRT

ORGANIEM: Candida albicans

US-10-741-849-7251
                                                                                                                                                                                          Query Match
Best Local Similarity 100.
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
US-60-495-114-1576
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139 SVEVEY 144
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192 VDVEY 196
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US-10-389-647-692
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Gaps

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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REPERENCE: CLOO0728

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR PELIOR DATE: 1999-10-05

PRIOR PELING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOOTWARE: FREESQ for Windows Version 4.0

SEQ ID NO 36165
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GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Orbin, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Heaing, Joseph E.
APPLICANT: Heaing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Malvas M. Slater, Sla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 26; DB 5; Length 303;
100.0%; Pred. No. 2.3e+03;
.ive 0; Mismatches 0; Indels
                                                                                                                                                             US-09-614-150A-36165
; Sequence 36165, Application US/09614150A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5; Conservative
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CRGANISM: Xenorhabdus sp. US-09-897-516A-6610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 VDVEY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-614-150A-36165
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APPLICANT: Spadera, Steven K
APPLICANT: Spadera, Steven K
APPLICANT: Spadera, Richard A.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers Padigaru
APPLICANT: Shinkers Padigaru
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REPERENCE: 15966-620 CIP
CURRENT APPLICATION NUMBER: US/10/701,283
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,564
PRIOR PILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR PILING DATE: 2000-01-04
PRIOR PILING DATE: 2000-01-07
PRIOR PELING DATE: 2000-01-07
PRIOR PILING DATE: 2000-01-07
PRIOR PILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN VET: 2.0
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86.7%; Score 26; DB 6; Length 285
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PLING DATE: 1090-10-4
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR PILING DATE: 2000-01-07
PRIOR PILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PARCHITIN Ver. 2.0
LENGTH: 284
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US-10-701-283-12
; Sequence 12, Application US/10701283
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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2 AVDIEY 7
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; ORGANISM: Hon
US-10-701-283-12
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1 SVDVEY 6

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193 AVDIEY 198
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US-10-415-182A-2698
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US-10-425-114A-40092
Sequence 40092, Application US/10425114A
Sequence 40092, Application US/10425114A
Sequence 40092, Application US/10425114A
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Aboult, David K.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Pabaska, Jack E.
APPLICANT: All Sand Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(3313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40092
LENGTH: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64094
LENGTH: 241
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86.7%; Score 26; DB 5; Length 316; 66.7%; Pred. No. 2.3e+03; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 26; DB 6; Length 341; 100.0%; Pred. No. 2.4e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3354-084-A4_FLI.pep
US-10-425-114A-64094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: 700995187_FLI.pep
US-10-425-114A-40092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 28
US-10-425-114A-64094
; Sequence 64094, Application US/10425114A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 5; Conservative
                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
                                                                                                                        |||::|
185 SVDIDY 190
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SVDIQY 64
                                                                                            1 SVDVEY 6
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ORGANISM: Zea mays
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208 VDVEY 212

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Sequence 982, Application US/10415182A
GENERAL INFORMATION:
APPLICANT: Telford. John
TITLE OF INVENTION:
CURRENT REPERENCE:
CURRENT PAPLICATION NUMBER: US/10/415,182A
CURRENT FILING DATE: 2003-12-09
PRIOR APPLICATION NUMBER: GB-002633.5
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-24
PRIOR FILING DATE: 2000-11-24
PRIOR FILING DATE: 2000-11-34
PRIOR FILING DATE: 2000-11-34
PRIOR FILING DATE: 2000-10-30-7
NUMBER OF SEQ ID NOS: 12024
SOFTWARE: SEQ ID NOS: 12024
IENGTH, 408
RESULT 29

US-10-739-930-10318

US-10-739-930-10318

US-10-739-930-10318

Sequence 10318, Application US/10739930

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT APPLICATION NUMBER: US/10/739,930

WUMBER OF SEQ ID NOS: 11088

SEQ ID NO 10318

LENGTH: 366
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GENERAL INFORMATION:
APPLICANT: Telford, John
TILLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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66.7%; Pred. No. 2.6e+03;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C3611_1.p
US-10-739-930-10318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 26; DB 6; Le
100.0%; Pred. No. 2.5e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(366)
OTHER INFORMATION: unsure at all Xaa locations FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus agalactiae.
US-10-415-182A-9892
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KBY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.77
Matches 4; Conservative
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Sequence 5786, Application US/10739930
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: UNCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: UNMER: US/10/739,930
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 5786
LENGTH: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
APPLICANT: Laurie, Cathy C
APPLICANT: Lebeaux, John R
APPLICANT: Fabbri, Brandon J
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Protein in Plants
FILE REFERENCE: 38-2153372)A
CURRENT PELLICATION NUMBER: US/60/479,962
CURRENT FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 488
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 442
                                                                                                                                                                                                                     Gaps
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| COCATION: (81)...(81)
| OTHER INFORMATION: Xaa can be any naturally occurring amino acid
| FEATURE:
| NAME/KEY: misc_feature
| COCATION: (304)...(304)
| OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-479-962-447
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0
  ) ORGANISM: Homo sapiens

) FRATURE:

) NAME/KEY: misc_feature

) OTHER INFORMATION: Incyte ID No: LI:200704.1.orf3:2001MAY17

US-10-473-040-683
                                                                                                                                                            Score 26; DB 6; Length 428;
Pred. No. 2.6e+03;
2; Mismatches 0; Indels
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100.0%; Pred. No. 2.6e+03;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 447, Application US/60479962
GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                         1 SVDVEY 6
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ORGANISM: Zea mays
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APPLICANT: LAN, RAKHAN, MICHAEL E.
ITILE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFRERENCE: PT-1231 USN
CURRENT APPLICATION UNMER: US/10/473,040
CURRENT FILING DATE: 2003-09-26
PRIOR PLICATION NUMBER: US/10/9944
RIOR FILING DATE: 2003-03-29
PRIOR PLICATION NUMBER: 60/299,619
PRIOR PLILING DATE: 2001-03-29
PRIOR PLILING DATE: 2001-05-16
PRIOR PLILING DATE: 2001-05-17
PRIOR PLILING DATE: 2001-06-17
PRIOR PLILING DATE: 2001-06-19
PRIOR PLILING DATE: 2001-06-20
NUMBER: 06/299,776
PRIOR PLILING DATE: 2001-06-20
NUMBER: OF SEQ ID NOS: 792
SOFTWARE: PERL PROGRAM
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APPLICANT: INCYTECT
APPLICANT: JONES, Anissa L.; TRAN, Alanna-Phung B.;
APPLICANT: JONES, Anissa L.; TRAN, Alanna-Phung B.;
APPLICANT: CHINN, JOYCE; DUFOUR, GERAIG E.;
APPLICANT: CHINN, JONIE, DUFOUR, GERAIG E.;
APPLICANT: JAKSON, Olivia; YAP, Pierre E.;
APPLICANT: ANSHEY, Stefan R.; DAUGHERTY, Sean C.;
APPLICANT: DAW, Tam C.; LIU, Tommy F.;
APPLICANT: MGTREN, DUY-Viet A.; KLEEFELD, Yael;
APPLICANT: GERSTIN, JR., Edward H.; PERALTA, Careyna H.;
APPLICANT: CHEN, Alice J.; PANZER, Scontt R.;
APPLICANT: HARRIS, Bernard; MULLAHY-FLORES, Vincent Z.;
APPLICANT: MARWAHA, Rakesh; LO, Audrey;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                           86.7%; Score 26; DB 6; Length 420
66.7%; Pred. No. 2.6e+03;
.ive 2; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/415,182A
CURRENT FILING DATE: 2003-12-09
PRIOR APPLICATION NUMBER: GB-002633.5
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-24
PRIOR PLING DATE: 2000-11-24
PRIOR PLING DATE: 2000-11-24
PRIOR PLING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 1203-6
SOFTWARE: SEQWIN99, Version 1.02
LENGTH: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 683, Application US/10473040 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         , OKGANISM: Streptococcus agalactiae
US-10-415-182A-2698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 428
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2707, Application US/10679063 GENERAL INFORMATION:
                                                                                                                                                          TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.78;
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Best Local Similarity 66.7
Matches 4; Conservative
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ORGANISM: Glycine max
US-10-679-063-2707
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204 AVDIEY 209
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US-10-451-168-56
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GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
ITTLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
        Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSGENCE PLANTS WITH IMPROVED PHENOTYPES
TITLE OF INVENTION: TRANSGENCE PLANTS WITH IMPROVED PHENOTYPES
TITLE REFERENCE: 38-15(32054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 16687
LENGTH: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2191. Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITL. OP INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
TITL. OP INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (5.2054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT APPLICATION NUMBER: 60415,758
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.7%; Score 26; DB 6; Length 460; 100.0%; Pred: No. 2.7e+03; ive 0; Mismatches 0; Indels
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          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i LOCATION: (1)..(532)
i OTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-2191
          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT / ORGANISM: Magnetospirillum magnetotacticum US-10-679-063-16687
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Best Local Similarity 66./
Best Local 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 5; Conservative
          5; Conservative
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                                                                        345 VDVEY 349
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42 VDVEY 46
                                              2 VDVEY 6
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                                                                                                                                              RESULT 35
US-10-679-063-16687
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US-10-472-928-3056
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US-10-679-063-2191
          Matches
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OTHER INFORMATION: phosphoglucomutase (pgm)
OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15903394 (0.E+01)
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION WIMBER: US/10/679,063
CURRENT TILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 2707
LENGTH: 597
                                                                                                                                                 Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 6; Length 597;
Pred. No. 2.9e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                           0; Indels
                                                                                                                                              Query Match

86.7%; Score 26; DB 6; 1

Best Local Similarity 66.7%; Pred. No. 2.9e+03;

Matches 4; Conservative 2; Mismatches 0
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GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION:
APPLICANT: SMITHKLINE BEECHAM D.1.c.
APPLICANT: GLAXO GROUP LIMITED
ITILE OF INVENTION: NOVEL COMPOUNDS:
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT PELING DATE: 2003-11-12
FRIOR APPLICATION NUMBER: PCT/US01/49232
FRIOR APPLICATION NUMBER: 60/256,710
FRIOR APPLICATION NUMBER: 60/256,710
FRIOR APPLICATION NUMBER: 60/256,710
FRIOR PILING DATE: 2000-12-17
FRIOR APPLICATION NUMBER: 60/256,70
FRIOR PELING DATE: 2001-12-0
FRIOR FILING DATE: 2001-01-09
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APPLICANT:
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOO728
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR PAPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-11-228
PRIOR PILING DATE: 1999-11-228
PRIOR PLILNG DATE: 1999-11-228
PRIOR PLILNG DATE: 2000-01-12
PRIOR PLILNG DATE: 2000-01-12
PRIOR PLILNG DATE: 2000-03-23
NUMBER: 60/191,637
PRIOR PLILNG DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRASSEQ for Windows Version 4.0
SEQ ID NO 18810
LENGTH: 615
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/19,637
PRIOR APPLICATION NUMBER: 60/19,637
PRIOR PLING DATE: 2000-02-33
NUMBER OF SEQ ID NOS: 43008
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                 Sequence 18810, Application US/09614150A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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US-09-614-150A-18810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 26; DB 6; Length 606
66.7%; Pred. No. 2.9e+03;
iive 2; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/266,/2/
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40

US-10-451-168-57

Sequence 57, Application US/10451168

GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS-039
CURRENT PELING DATE: 2003-11-2
PRIOR APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-12-09
PRIOR FILING DATE: 2001-12-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2002-06-05
PRIOR FILING PRIOR FILING PRIOR FILING PRI
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-451-168-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 ŠIĎLĖY 581
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576 SIDLEY 581
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US-09-614-150A-18810
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Gaps

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Sequence 167, Application US/10475292
GENERAL INFORMATION:
APPLICANT: AI XioLan et al.
TITLE OF INVENTION: PRIMARY NUCLECTIDE SEQUENCE OF THE
TITLE OF INVENTION: AGROTIS SEGETUM GRANULOSIS VIRUS (AsGV), INSECTICIDE
TITLE OF INVENTION: ADD CONTROLLING KITS FOR AGROTIS SEGETUM INSECT OUTBREAK AND
TITLE OF INVENTION: SPREAD
TITLE OF INVENTION: SPREAD
FILE REFERENCE: CL001308-US
CURRENT PRILING DATE: 2003-10-20
FRIOR APPLICATION NUMBER: DCT/US01/32153
FRIOR PLING DATE: 2001-10-17
FRIOR PLING DATE: 2001-10-17
FRIOR RILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 217
SEQ ID NO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BARA, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGTUS, CATHERINE T.
APPLICANT: MALB.
APPLICANT: WASHERTE, MAL B.
APPLICANT: WEBB, ELIZABETH A.
TITLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/581,286A
CURRENT APPLICATION NUMBER: BCT/AU98/01023
FRIOR PELING DATE: 1998-12-13
PRIOR APPLICATION NUMBER: AU PP 0839
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: AU PP 182
PRIOR APPLICATION NUMBER: AU PP 1846
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-04-09
PRIOR FLING DATE: 1998-04-09
PRIOR FLING DATE: 1998-04-23
PRIOR FLING DATE: 1998-04-23
PRIOR FLING DATE: 1998-04-23
PRIOR FLING DATE: 1998-04-23
PRIOR RELING DATE: 1998-04-23
PRIOR FLING DATE: 1998-04-23
PRIOR RELING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: AU PP 3338
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66.7%; Pred. No. 3.3e+03;
ive 2; Mismatches 0; Indels
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                Pred. No. 3e+03;
100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                              5, Conservative
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      Best Local Similarity
Matches 5, Conserv
                                                                                                                                                  217 VDVBY 221
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                                                                                                          2 VDVBY 6
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US-09-581-286A-442
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                                                                                                                                                                                                                                                                       RESULT 45
US-10-475-292-167
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Sequence 42, Application US/10418861B

GENERAL INFORMATION:
APPLICANT: Farah, Shaker Chuck
APPLICANT: Reinach, Fernando de Castro
APPLICANT: Reinach, Fernando de Castro
APPLICANT: Reinach, Fernando de Castro
APPLICANT: Belach, Marcelo Luiz
APPLICANT: De Laia, Marcelo Luiz
APPLICANT: Belach and Joan C.
APPLICANT: Setubal Joan C.
APPLICANT: Setubal Joan C.
APPLICANT: Bolated Xanthomonas nucleic acid molecules, proteins encoded the TILE De INVENTION: 1804 thereof
FILE REFERENCE: PAPESP 205.1 US
CURRENT FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-22
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 42
LENGTH: 676
LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 106, Application US/60495589
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Progulske-Fox, Ann
APPLICANT: Progulske-Fox, Ann
APPLICANT: Halflan, Deffrey D.
APPLICANT: Deffrey D.
APPLICANT: Halflan, Deffrey D.
APPLICANT: Deffrey D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 7; Length 673; 83.3%; Pred. No. 3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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                                                                      TYPE: PRT ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 SVDVEF 390
                                                                                                                                                                                                                                                                                                                                                                                            449 SIDVDY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                1 SVDVEY 6
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                                                                                                                                     US-09-614-150A-3981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 43
US-60-495-589-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 44
US-10-418-861B-42
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      SEQ ID NO 3981
LENGTH: 633
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459 TVDIEY 464
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GENERAL INFORMATION:
APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAM G.
APPLICANT: PATTERSON MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: MALB J.
APPLICANT: MEBB. ELIZABETH A.
APPLICANT: WEBB. ELIZABETH A.
APPLICANTON UNMER: US/09/581,286A
CURRENT FILING DATE: 1999-12-10
FRIOR PLING DATE: 1999-12-10
FRIOR APPLICANTON UNMER: AU PP 1182
FRIOR APPLICANTON UNMER: AU PP 1182
FRIOR APPLICANTON UNMER: AU PP 2264
FRIOR APPLICANTON UNMER: AU PP 2264
FRIOR FILING DATE: 1998-03-10
FRIOR APPLICANTON UNMER: AU PP 2318
FRIOR FILING DATE: 1998-03-10
FRIOR APPLICANTON UNMER: AU PP 3128
FRIOR FILING DATE: 1998-03-10
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 354
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 354
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 354
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 354
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 354
FRIOR FILING DATE: 1998-07-39
FRIOR FILING DATE: 1998-07-39
FRIOR FILING DATE: 1998-07-30
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-07-29
PROR FILING DATE: 1998-07-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 721
SEQ ID NO 442
LENGTH: 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.7%; Score 26; DB 5; I
66.7%; Pred. No. 3.3e+03;
iive 2; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 316, Application US/09581286A, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Porphyromonas gingivalis US-09-581-286A-442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . TYPE: PRT
. ORGANISM: Porphyromonas gingivalis
US-09-581-286A-316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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451 TVDIEY 456
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US-10-472-928-972
Sequence 972, Application US/10472928
Sequence 972, Application US/10472928
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
TILLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: B026926WO
CURRENT FILING DATE: 2003-92-26
PRIOR PELICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWing9, version 1.03
EDNOTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

83.3%; Score 25; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: RESESEQ for Windows Version 4.0
LENGTH: 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Streptococcus pneumoniae
FEATURE:
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-18237
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122 TVDIEY 127
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26 VDIEY 30
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Search completed: January 20, 2004, 14:01:56 Job time : 25 secs

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Scoring table:

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score:

Sequence:

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Sequence 5, Applisequence 6, Applisequence 7, Applisequence 1266, Asplisequence 1266, Applisequence 1266, Applisequence 1266, Applisequence 12, Applisequence 12, Applisequence 12, Applisequence 12, Applisequence 12, Applisequence 25, Applisequence 216, Applisequence 2166, Asequence 2166, Asequence 2161, Applisequence 2166, Asequence 2161, Applisequence 2161, Ap
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Sequence 13, Appl
Sequence 53090, A
Sequence 6887, Ap
Sequence 6887, Ap
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Sequence 1, Appli
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                                                                                                                 ; Search time 173 Seconds (without alignments) 31.558 Million cell updates/sec
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1: (cgn12 6/ptodata/1/paa/USO6 COMB.ppp: *

2: (cgn2 6/ptodata/1/paa/USO6 COMB.ppp: *

4: (cgn2 6/ptodata/1/paa/USO8 COMB.ppp: *

5: (cgn2 6/ptodata/1/paa/USO81 CCMB.ppp: *

6: (cgn2 6/ptodata/1/paa/USO81 CCMB.ppp: *

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18: (cgn2 6/ptodata/1/paa/USO97 CCMB.ppp: *

19: (cgn2 6/ptodata/1/paa/USO98 CCMB.ppp: *

10: (cgn2 6/ptodata/1/paa/USO99 CCMB.ppp: *

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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 75 summaries
                                                                                     protein search, using sw model
                                                                                                                     2004, 13:55:27
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-919-703-5

US-09-919-703-5

Sequence 5, Application US/09919703

GENERAL INFORMATION:
APPLICANT: RAYSHAI, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
TITLE OF INVENTION: Peptides and Their Use to Ameliorate;
TITLE REFERENCE: 50216/003004

CURRENT FILING DATE: 1099-04-19

PRIOR PELICATION NUMBER: US 09/294,457

PRIOR PELICATION NUMBER: US 09/294,457

PRIOR PELICATION NUMBER: US 08/759,599

PRIOR FILING DATE: 1999-04-19

PRIOR FILING DATE: 1995-12-06

NUMBER: OF SEQ ID NOS: 16

SEQ ID NO S: LENGTH: 1000-12-12-06

LENGTH: 16

LENGTH: 16
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GENERAL INFORMATION:
APPLICANT: Rabkin, Simon W.
APPLICANT: Rabkin, Simon W.
APPLICANT: RAPKIN, Simon W.
APPLICANT: RAPKIN, Simon W.
APPLICANT: RABKIN, SIMON WOVEL PEPTIDES AND THEIR USE TO TITLE OF INVENTION: AMELIORATE CELL DEATH NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                ;
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100.0%; Pred. No. 5.3e+06;
tive 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                CTHER INFORMATION: Synthetic polypeptide US-09-919-703-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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       Sequence 3, Appli
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APPLICANT: Kryerian, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1996-12-05
PRIOR FILING DATE: 1996-12-05
PRIOR FILING DATE: 1995-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 9; Length 6; Pred. No. 5.3e+06;
                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Rabkin, Simon W.

APPLICANT: Rabkin, Simon W.

APPLICANT: Rabkin, Simon W.

APPLICANT: Rabkin, Simon W.

TITLE OF INVENTION: AMELIORATE CELL DEATH

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: SEED and BERRY

STREET: 8300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/567,943

FILING DATE: 06-DEC-1995

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: MCMSETERS DAVID D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 31

TELEPHONE: (206) 682-6031

TELEX: 372336

INFORMATION FOR SEQ ID NO: 1:

SECUENCE CHARACTERISTICS:

LENGTH: SAINGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
       US-09-919-703-3
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                                                                          ALIGNMENTS
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US-09-919-703-1
Sequence 1, Application US/09919703
GENERAL INFORMATION:
                                                                                                                                                                                        Sequence 1, Application US/08567943 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 6; Conservative 0;
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1 SVDVEY 6
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                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09919703
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/00304
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENTH: 20
                                     Query Match
100.0%; Score 30; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rabkin, Simon W.
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE SIES
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 99104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,943
FILING DATE: 06-DEC-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08567943 GENERAL INFORMATION:
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NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
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100.0%; Score 30; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,943
FILING DATE: 06-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCMESTERS 33,963
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
TELEPRAN: (206) 622-4900
TELEPRAN: (206) 622-4900
TELEPRAN: (206) 622-4900
TELEPRAN: (206) 622-6031
TELEPRAN: RS GO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TTELENTY: amino acids
TTELENTY: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rabkin, Simon W.
APPLICANT: Rabkin, Simon W.
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 22ED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTX: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,943
FILING DATE: 06-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REBERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
RELEPAN: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08567943 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
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STRANDEDNESS: single
TOPOLOGY: linear
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US-08-567-943-6
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Gaps

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Sequence 12562, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomia, inc.
APPLICANT: Debe, Derek
APPLICANT: Denser, Joseph
ITILE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
ITILE OF INVENTION: METHODS OF USE THEREOF
ITILE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
SOFTWARE PARENTING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE PARENTIN VERSION 3.0
SEQ ID NO 12562
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Sequence 10448, Application US/09791537

GENERAL INFORMATION.

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

TITLE OF INVENTION: TRREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB)

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT PILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE PATENTIN VERSION 3.0

SEQ ID NO 104248

LENGTH: 138
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                                                                                                             Score 30; DB 22; Length 128;
Pred. No. 1.3e+02;
                                                                                                                                                          0; Indels
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                                                                                                                                                          0; Mismatches
                        TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-83460
                                                                                                                100.0%;
100.0%;
                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: pdb 1C4PA
US-09-791-537-12562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: pdb 1QORA
US-09-791-537-104248
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US-09-791-537-12562
        LENGTH: 128
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GENERAL INFORMATION:
APPLICANT: Bilonomix, Inc.
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PARCHIN VETSION 3.0
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; Sequence 7, Application US/09919703
; GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: SO216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR PRILOR DATE: 1999-04-19
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 21
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REFERENCE/DOCKET NUMBER: 780059.401A1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTER.STICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                              ESS: single
linear
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US-09-791-537-83460
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TOPOLOGY:
US-08-567-943-7
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US-09-919-703-7
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GENERAL INFORMATION:
APPLICANT: Rabkin, Simon W.
APPLICANT: Krystal, Gerald
ITILE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELICRATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Madrazo, Isis Del Carmen Torrens
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Menendez, Alina Seralena
APPLICANT: Escalona, Blder Pupo
APPLICANT: Escalona, Blder Pupo
APPLICANT: Gariego, Martha De Jesus Gonzalez
APPLICANT: Gariego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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100.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/658,681
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 384
                                                                                                                                           TYPE: PRT / ORGANISM: Streptococcus equisimilis US-09-658-681-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09658681 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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ZIP: 98104-7092
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                                                                                        APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN version 3.0
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Glalvo, Ariana Garcia
APPLICANT: Olalvo, Ariana Garcia
APPLICANT: Memendez, Alina Seralena
APPLICANT: Bscalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
ITILE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
CURRENT APPLICATION UNMBER: US/09/658,681
CURRENT APPLICATION UNMBER: US/09/658,681
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SSEQ ID NOS: 14
SSEQ ID NO 3: 12
LENGTH: 372
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100.0%; Pred. No. 4.6e+02;
ive 0; Mismatches 0;
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Ojalvo, Ariana Garcia
APPLICANT: Menendez, Alina Seralena
APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPPOKITASE WITANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
                   Sequence 23287, Application US/09791537 GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Streptococcus equisimilis US-09-658-681-3
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Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: pdb 1BMLC
US-09-791-537-23287
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Matches 6; Conserv
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    US-09-791-537-23287
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LENGTH: 362
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US-09-658-681-4
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Gaps

. 0

0; Indels

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100.0%; Score 30; DB 24; Length 413; 100.0%; Pred. No. 5.4e+02;
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PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Synthetic polypeptide US-09-919-703-12
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 SVDVEY 161
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PCT-US93-09502-1
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SEQUENCE 12, Application US/09919703

SEQUENCE 12, Application US/09919703

SEQUENCE 11 SECONDARY OF SECONDARY OF
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Sequence 2, Application US/09658681
Sequence 2, Application US/09658681
Sequence 2, Application US/09658681
Sequence 2, Application US/09658681
APPLICANT: Madrazo, Isis Del Carmen Torrens
APPLICANT: Gjalvo, Ariana Garcia
APPLICANT: Menendaz, Alina Soralena
APPLICANT: Mescalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Marcha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REPRENCE: Sequence Listings 1-14 re: 976-5
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
FINGTH: APPLICATION OF CONTROL OF CONTROL
     APPLICALLE.
FILING DATE: 06-DEC-LJJC
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCAMBER: 33,963
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401A1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFACH. (206) 622-631
TELEFACH. (206) 62-631
TELEFACH. (206) 62-631
TELEFACH. (206) 62-631
TELECOMUNICATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 amino acids
TYPE: amino acid
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; ORGANISM: Streptococcus equisimilis
US-09-658-681-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
Matches 6; Conserva
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Gegreence 264, Application US/10360101
GENERAL INFORMATION:
APPLICANT: Holl, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT PILING DATE: 2002-05-24
NUMBER: OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 264
LIBRICH: 413
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GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the TITLE OF INVENTION: DAM Encoding Such Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein and Fox
STREET: 1100 New York Avenue, Suite 600
STATE: D.C.
COUNTRY: U.S.A.
STREET: D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: sequence of streptokinase US-10-360-101-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Reed, Guy L.
APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the TITLE OF INVENTION: DNA Encoding Such Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Sterne, Kessler, Goldstein and Fox STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.25
SOUTHARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/128,299
FLING DATE: Herewith
CLASSIFICATION 435
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REFERENCE/DOCKET NUMBER: 0609.3570001
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2560
TELEFAX: (202) 371-2545
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENNEYAL 414 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARE INFORMATION.
APPLICANT: CARR, Francis Joseph
ADAIR, Fiona Suzanne
HAMILTON, Anita Anne
CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
NON-IMMUNOGENIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 30; DB 5; I 100.0%; Pred. No. 5.4e+02;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr L.L.P.
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 252, Application US/09438136 GENERAL INFORMATION:
                                                                                                                                                                                             Sequence 1, Application US/08128299 GENERAL INFORMATION:
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COUNTRY: United States
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COMPUTER READABLE FORM:
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TYPE: amino acid
STRANDEDNESS: both
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Matches 6, Conservative
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                                                                        157 SVDVEY 162
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US-09-438-136-252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Guy L.
APPLICANT: Reed, Guy L.
APPLICANT: Reed, Guy L.
APPLICANT: Parhami-Seren, Behnaz
TITLE OF INVENTION: Recombinant Streptokinase Fragments with
TITLE OF INVENTION: Decreased Antigenicity and Uses Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox
STREET: 1225 Connecticut Avenue
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%; Score 30; DB 3; Length 414;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TERE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: The PC compatible
COMPATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT APPLICATION DATE: 19921005
FLING DATE: 19921005
FREDENCK-COCKET NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3570000
FELEPHONE: (202) 833-7533
FELEPHONE: (202) 833-753
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09502
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                               0609.3570001
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                                                                                       CLASSIFICATION:
CLASSIFICATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-260
TELEFAX: (202) 371-260
TELEFAX: (202) 371-265
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 414 amino acids
TYPE: AMINO ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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Best Local Similarity
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PCT-US93-09502-1
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US-07-953-692A-9
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US-07-956-692A-9
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Sequence 2, Application US/09471349
GENERAL INFORMATION:
APPLICANT: Sahni, Girish
APPLICANT: Rumar, Rajesh
APPLICANT: Roy, Chait
APPLICANT: Ray agopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
ITILE OF INVENTION: PLASHINGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF SAID PROTEINS
FILE REFERENCE: 07064/009001
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                                                FILING DATE: 21-WAY-1997

PILING DATE: 21-WAY-1997

PILING DATE: 31-JUL.1997

APPLICATION NUMBER: GB 9716197.0

PILING DATE: 28-NOV-1997

APPLICATION NUMBER: GB 960751.4

PILING DATE: 14-APR-1998

APPLICATION NUMBER: US 60/067,235

FILING DATE: 02-DEC-1997

ATORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.

REFERENCE/POCKET NUMBER: 102286.395CON

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 18;
100.0%; Pred. No. 5.4e+02;
iive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: U509/471,349
CURRENT FILING DATE: 1999-12-23
FRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
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                                  9710480.6
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SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-438-136-253
                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 526-6000 INFORMATION FOR SEQ ID NO: 253:
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US-09-633-516B-7
; Sequence 7, Application US/09633516B
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,136
FILING DATE: 10-Nov-1999
CLASSIFCATION NUMBER: WO PCT/GB98/01473
FILING DATE: 21-MAY-1998
APPLICATION NUMBER: GB 9710480.6
FILING DATE: 21-MAY-1997
APPLICATION NUMBER: GB 9716197.0
FILING DATE: 31-JUL-1997
APPLICATION NUMBER: GB 9725270.4
FILING DATE: 28-NOV-1997
APPLICATION NUMBER: GB 9725270.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: GB 9725270.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: B 9807751.4
FILING DATE: 14-APR-1998
ARPLICATION NUMBER: US 60/067,235
ATTORNEY/AGENT INFORMATION:
NAME: Baker, HOllie L.
REGISTRATION NUMBER: 31,321
REFRENCE/DOCKET NUMBER: 102286.395CON
TELERCOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,136
FILING DATE: 10-Nov-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 253, Application US/09438136
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APALICANT: CARR, From Suzanne
HAMILTON, Anita Anne
CARTER, Graham
TITLE OF INVENTION: NETHOD FOR THE PRODUCTION OF
NON-IMMUNOGENIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB98/01473
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SEQUENCE DESCRIPTION: SEQ ID NO: 252:
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ADDRESSEE: Hale and Dorr L.L.P.
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 526-6000 INFORMATION FOR SEQ ID NO: 252:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COUNTRY: United States
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Best Local Similarity
Matches 6; Conserva
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US-09-438-136-253
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Gaps

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APPLICANT: Dataer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITILE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITILE OF INVENTION: METHODS OF USE THEREOF
FILE REFRENCE: 261/210/21/237
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 418
LENGTHRE: PATENTIN VERSION 3.0
SEQ ID NO 418
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GENERAL GEN
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100.0%; Pred. No. 5.4e+02;
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GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fions Suzanne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Streptococcus equisimilis US-09-791-537-418
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Best Local Similarity 100.
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APPLICANT: Bionomix, Inc.
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Frona Suzanne ADAIR
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
TILLE OF INVENTION: Modifying Protein Immunogenicity
FILE REPERENCE: 112408-120
CURRENT APPLICATION NUMBER: US/09/633,516B
2000-08-04
CURRENT APPLICATION NUMBER: PCT/GB99/04119
PRIOR APPLICATION NUMBER: GB992695.1
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: GB9902139.6
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: GB9902139.6
PRIOR FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
                      APPLICANT: Francis Joseph CARR
APPLICANT: Froma Suzanne ADAIR
APPLICANT: Anita Anne HAMILTON
APPLICANT: Graham CARTER
TITLE OF INVENTION: Modifying Protein Immunogenicity
FILE REPERENCE: 112408-120
CURRENT APPLICATION NUMBER: US/09/633,516B
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                                                                                                                                                                                                                               RESULT 28
US-09-791-537-418
; Sequence 418, Application US/09791537
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus equisimilis
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Sequence 2, Application US/10631558
GENERAL INFORMATION:
APPLICANT: Rumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Rajespal, Kammara
APPLICANT: Rajespal, Kammara
APPLICANT: Rajespal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: NoveL CLOT-SPECIFIC STREPTOKINASE
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASHINOGEN ACTIVATION
ITILE OF INVENTION: PROTEINS
ITILE OF INVENTION: PROTEINS
ITILE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
ITILE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
ITILE OF INVENTION: UNMBER: US/10/631,558
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US/09/940,235
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 144
TAYDE: DOTAL
                          Gaps
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APPLICANT: Zhang, Xuejun C
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
TITLE OF INVENTION: Thrombolytic Agents Derived from Streptokinase
FILE REFERENCE: OMRF 173
CURRENT APPLICATION NUMBER: US/09/305,958
CURRENT APPLICATION NUMBER: 60/084,392
EARLIER APPLICATION NUMBER: 60/084,392
EARLIER FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 415
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100.0%; Score 30; DB 31;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0;
100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Streptococcus equisimilis US-10-631-558-2
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US-09-305-958-4
; Sequence 4, Application US/09305958
; GENERAL INFORMATION:
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NAME/KEY: PEPTIDE
CCATION: (1)...(415)
CCTHER INFORMATION: Etreptokinase
US-09-305-958-4
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ORGANISM: Streptococcus sp
Best Local Similarity 100. Matches 6; Conservative
                                                                                                                  157 SVDVEY 162
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                                                                                  1 SVDVEY 6
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GENERAL INFORMATION:
APPLICANT: ADAR, Frience Suzanne
APPLICANT: ADAR, Filona Suzanne
APPLICANT: ADAR, Filona Suzanne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: ANITA Anne
TITLE OF INVENTION: MON-IMMUNGENIC PROUCTION OF
TITLE OF INVENTION: MON-IMMUNGENIC PROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT APPLICATION NUMBER: US/10/300,215
CURRENT APPLICATION NUMBER: US/04/38,136
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR PLING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR PELING DATE: 1999-05-21
PRIOR PELING DATE: 1997-07-31
PRIOR PELING DATE: 1997-11-28
PRIOR PELING DATE: 1997-11-28
PRIOR PELING DATE: 1997-11-28
PRIOR PELING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 254
NUMBER OF SEQ ID NOS: 254
LENGTH: 414
                    FILE REFERENCE: MER-104-Con.1
CURRENY APPLICATION NUMBER: US/10/300,215
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1998-05-21
PRIOR PILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR PILING DATE: 1997-05-21
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR APPLICATION NUMBER: GB 9725270.4
PRIOR PILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-11-28
PRIOR FILING DATE: 1997-11-28
PRIOR FILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-44
PRIOR PILING DATE: 1997-11-02
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 252
LENGTH: 414
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS
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; ORGANISM: Streptococcus equisimilis
US-10-300-215-252
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Best Local Similarity 100.
Matches 6; Conservative
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DB 29; Length 414;

100.0%; Score 30;

Query Match

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Sequence 45187, Application US/09791537
GREEAL INFORMATION:
APPLICANT: Bionomix. Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOOFWARE: Patentin version 3.0
SEQ ID NO 45187
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, 1nc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
APPLICANT: 201-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARR: Patentin version 3.0
SEQ ID NO 45189
LENGTH: 440
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBYCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Ratentin version 3.0
SEQ ID NO 45192
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; ORGANISM: Streptococcus equisimilis
US-09-791-537-45187
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-791-537-45192
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Petentin version 3.0
SEQ ID NO 32688
LENGTH: 415
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Query Match 100.0%; Score 30; DB 17; Length 415; Best Local Similarity 100.0%; Pred. No. 5.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Human Plasminogen Activator
TITLE OF INVENTION: Human Plasminogen Activator
FILE REFERENCE: OMRF 175
CURRENT APPLICATION NUMBER: US/09/305,970
CURRENT PILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/110,588
EARLIER FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
IENGTH: 415
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100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0;
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   ORGANISM: Streptococcus equisimilis
US-09-791-537-32688
                                                                                                                                                                                                                          RESULT 34
US-09-305-970-5
; Sequence 5, Application US/09305970
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(415)
; OTHER INFORMATION: streptokinase
US-09-305-970-5
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TPLE DEDIZER, JOSEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 145994
LENGTH: 891
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                                                                                                                                                                                              APPLICANT: Martin R.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Miliamen, Mark
TITLE OF INTENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: MPI1999-096CP2
CURRENT APPLICATION NUMBER: US/09/609,360D
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/562,480
PRIOR RILING DATE: 1999-06-30
PRIOR RILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2: SEQ ID NOS: 90
LENGTH: 891
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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: Novel Kinases and Uses Thereof
PILE REFERENCE: 35800/234862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-791-537-145994
; Sequence 145994, Application US/09791537
; GENERAL INFORMATION:
                                                                                                                                                        Sequence 25, Application US/09609360D GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-609-360D-25
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; ORGANISM: Hydra vulgaris
US-09-791-537-145994
                                       137 SVDVEY 142
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1 SVDVEY
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US-09-609-360D-25
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US-09-862-027-25
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                                                                                                         100.0%; Score 30; DB 22; Length 440; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels (
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100.0%; Score 30; DB 20; Length 891;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09609360B

Sequence 25, Application US/09609360B

APPLICANT: Hodge, Martin R.
APPLICANT: Meyers, Rachart

TITLE OF INVENTION: Novel Rinases and Uses Thereof
FILE REFERENCE: 35800/200938

CURRENT FILING DATE: 2000-11-13

PRIOR PILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: US/09/609,360B

CURRENT FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-05-01

NUMBER: OF SEQ ID NOS: 83

NUMBER: OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 891
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GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Hodge, Martin R.
APPLICANT: Majlamson, Mark
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: MP11999-096CP2
CURRENT APPLICATION NUMBER: 09/9609,360C
CURRENT FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR PLILORION NUMBER: 09/345,473
PRIOR PLILOR DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 891
                     ; TYPE: PRT
; ORGANISM: Streptococcus sp
US-09-791-537-45192
                                                                                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Hydra vulgaris
US-09-609-360B-25
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US-09-609-360C-25
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 440
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                                                                                                                                                                                                                                         Sequence 234, Application US/60143753
GENERAL INFORMATION:
APPLICANT: Kerlawage, Anthony
APPLICANT: Kerlawage, Anthony
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION WUMBER: US/60/143,753
CURRENT FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 234
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-60-145-989-236

JS SEQUENCE 236, Application US/60145989

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES;

TITLE OF INVENTION: THERROF

FILE REFERENCE: CL000066

CURRENT APPLICATION NUMBER: US/60/145,989

CURRENT APPLICATION NUMBER: US/60/145,989

NUMBER OF SEQ ID NOS: 456

SEQ ID NO 236

LEMETH: 66

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           DB 32; Length 43;
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96.7%; Score 29; DB 32;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%; Score 29; DB 32;
83.3%; Pred. No. 56;
trive 1; Mismatches 0
        Score 29; DB :
Pred. No. 56;
1; Mismatches
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ORGANISM: Drosophila
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(66)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-145-989-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
COGANISM: Drosophila
FEATURE:
NAME/KEY: VARIANT
J. LOCATION: (1)...(43)
OCHER INFORMATION: Xaa = Any Amino Acid
US-60-143-753-234
        Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105510, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bloomaix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: AND MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: CLORO0035
CURRENT APPLICATION NUMBER: US/60/139,670
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 229
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 43
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                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 30; DB 23; Length 891; Best Local Similarity 100.0%; Pred. No. 1.4e+03; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: VARIANT;
) LOCATION: (1)...(43)
) OTHER INFORMATION: Xaa = Any Amino Acid
US-60-139-670-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Dunaliella salina
US-09-791-537-105510
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Hydra vulgaris
US-09-862-027-25
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ORGANISM: Drosophila
                                                                                                                                                                                                                                                                                                                                                         1 SVDVEY 6
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US-09-791-537-105510
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LENGTH: 1274
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US-60-139-670-115
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96.7%;
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Best Local Similarity 83.3
Matches 5; Conservative
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Avoil of David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF ENCENT OF THEREOF
CURRENT APPLICATION NUMBER: US/60/145,989
CURRENT APPLICATION NUMBER: US/60/145,989
NUMBER OF SEQ ID NOS: 456
SOFTWARE: FRAESEQ for Windows Version 3.0
SEQ ID NO 317
LENGTH: 68
  Sequence 515, Application US/60145138

Sequence 515, Application US/60145138

GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00062
CURRENT APPLICATION NUMBER: US/60/145,138
CURRENT FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 948
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 515
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                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KES:
COCATION: (1)...(69)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-145-138-515
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // TYPE: PRT
// ORGANISM: Drosophila
US-60-145-989-317
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38 SIDVEY 43
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US-10-424-599-271681
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US-60-145-989-317
US-60-145-138-515
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
; SEQ ID NO 271681
; LENGTH: 72
; TYPE: RRT
; ORGANISM: Glycine max
; FEATURE:
NAME/KEY: unsure
; LOCATION: (1)...(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87347C.1.pep
US-10-424-599-271681
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Streptokinase from Streptokinase (1-3 Recombiant strept Truncated Met stre Streptokinase (1-3

AAY01550
AAY01558
AAY01558
AAY01557
AAR10159
AAR10197
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AAR10197
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                                                      2004, 14:37:25 ; Search time 42 Seconds (without alignments) 22.675 Million cell updates/sec
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| SIDSI_gcgdata_geneseq_geneseq_embl/AA1981.DAT:*
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    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                      1107863 segs, 158726573 residues
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                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries
                                         protein search, using sw model
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ABB80001
AAY25013
AAY25014
ABB60006
ABG76055
AAY25015
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length: 2000000000
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Perfect score:
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AAY24794
AAY01556
AAW94665
AAW96143
AAW86144
AAY90282
AAB01295
AAB01295
AAB70295
AAR70870
AAY90593
AAY90593
AAY90593
AAY12885
AAR12885
AAR12885
AAR12882
AAR12882

ALIGNMENTS

AAU64792 ABG16037 AAW06741 ABR39091

ABB80003 ABG74195 AAY51961 AAY51973 ABP60417

AAY24797 AAW21723 AAW21728 AAR12893 AAW21724 AAW21726 AAW21726 ABB58817 AAY25011

Leptospira membran Galid herpesvirus

Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperhermia; hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; meurodegenerative disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; cardiorascular disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infaction; heart disease; rardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; perfusion injury; immune disease; rheumatoid arthritis; enthritius; perfusion injury; dermatomyositis; enythema nodosum; myasthenia gravis; perfusion anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome; meoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma; melanoma; cancer; breast; collon; cervix; prostate; Hodgkin's disease; non-Hodgkin's Lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; spinal and Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation Streptokinase derived peptide 1 for amelioration of cell death. peptides derived from Claim 2; Column 12; 15pp; English. AAY25009 standard; peptide; 6 AA 96US-0759599 95US-0008233 96US-0759599 (first entry) AAY25009-Y25019 are novel Krystal G, Rabkin SW; WPI; 1999-394231/33. (RABK/) RABKIN S W. 05-DEC-1996; 06-DEC-1995; 23-AUG-1999 05-DEC-1996; 29-JUN-1999 Synthetic. AAY25009;

(MOLE-) MOLECULAR THERAPEUTICS INC ABB80001 standard; peptide; 6 AA. Claim 3; Column 5; 18pp; English Streptokinase derived peptide#1. 100.0%; 95US-008233P. 26-JUL-2002 (first entry) 6; Conservative prion disease; aging WPI; 2002-266542/31. and anthracyclines. Query Match Best Local Similarity 9 6 AA; 1 SVDVEY SVDVEY JS6348567-B1. 19-APR-1999; 06-DEC-1995; 05-DEC-1996; 19-FEB-2002, Krystal G, Synthetic. ABB80001; Sequence Matches RESULT 2 ABB8000] a ઠે AMISOUSTICATORS ALE HOVEL DEPLACES OF THE INVENTIFY CALLIDATE LIBER CONTINUES CALCUSTICATIONS AND ALEST CALCUSTICATION OF THE INVENTIFY CALCUSTICATION OF THE INVENTIFY CALCUSTICATION OF THE INTENTITY CALCUSTICATION OF THE INSTITUTE CALCUSTICATION OF THE INSTITUTE CALCUSTICATION OF THE INSTITUTE CALCUSTICATION OF THE INTENTITY O

Streptokinase, cell death, apoptosis, necrosis, nootropic,
meuroprotective, antiparkhrsonian, antichnumatic, cardiant,
wantinflammatory; antiarkhritic; antichnumatic, cardiant,
wantiatherosclerotic; vasotropic; immunosuppressive, antithly
dermatological, antidiabetic; antianaemic; virucide, ophthalmological,
wantiulcer; antibacterial, antiparastlic; neurodegenerative disease;
wantiulcer; antibacterial, antiparastlic; neurodegenerative disease;
wathingen's disease, Alzheimer's disease; Huntington's disease;
wathingmatory disorder; arthritis, inflammatory joint disorders;
wathingmatory disorder; arthritis, inflammatory joint disorders;
wathous conder; arthritis, inflammatory joint disorders;
wathingmatory disorder; arthritis, inflammatory joint disease;
wathous erythematosus; diabetes mellitus; pernicious anaemia;
wathodegenerative diseases; ulcerative colitis; pancreatitis;
waterial Crohn's disease; ulcerative colitis; pancreatitis; ö other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia or infarction, and stroke), toxic insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxious substances), macular degeneration, cataract formation, pancreatitis, Crohn's disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT, Gaps New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders .. 0 Length 6; Indels ö ; Score 30; DB 20; ; Pred. No. 9.3e+05; 0; Mismatches 0;

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antiparkinsonian, anticonvulsant, cytostatic, antiatherosolarotic, vasotropic, immunosuppressive, anti-HNO described as antiuler, antiparentic, reptides of the invention antiuloer, antibacterial and antiparasitic. Peptides of the invention antiuloer, antibacterial and antiparasitic. Peptides of the invention antiparasitic peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. parkinson's, Altoeimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. arthitis, inflammatory joint and myocardial reperfusion injury), immune diseases (e.g. heart failure, atherosolerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases of systemic lupus erythematosus, diabetee mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases of any organ. Other disorders include macular degeneration, cataracts, croph, s diseases including bacteria, parasite, prion-based diseases, and accelerated aging. The current sequence repersents a streptokinase daring and any organ and allocation with an ability to ameliorate cell
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neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;
antiinflammatory; antiarthritic; antichneuralic, cardiant;
antiinflammatory; antiarthritic; antichneuralic, cardiant;
antiulers; antibacterial; antiparasitc; neurodegenerative disease;
A parkinson's disease; Alzheimer's disease; Huntington's disease;
A parkinson's disease; Alzheimer's disease; Huntington's disease;
A cardiovascular degeneration, neoplastic disorder; cancer;
antilammatory disorder; arthritis; inflammatory joint disorders;
A cardiovascular disease; arthritis; inflammatory joint disorders;
A cardiovascular disease; arthritis; inflammatory joint disorders;
A cardiovascular disease; arthritis; inflammatory disorders;
A myocardial repertusion injury; immune disease;
A myelodegenerative diseases; viral diseases; autoimmune disease;
A spetemic lupus erythematosus; diabetes mellitus; pernicious anaemia;
A cataract; Croh's diseases; varal diseases; macular degeneration;
A cataract; Croh's disease; varal diseases; macular degeneration;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80005 standard; peptide; 16 AA.
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96US-0759599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              death in cardiac myocytes.
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Best Local Similarity 100،۰
ادم و Conservative في Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prion disease; aging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA;
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05-DEC-1996;
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peptides or the invention may be described as, mostropic, antinflammatory, antiparkingonian, anticonvulant, cytostatic, antinflammatory, antiparkingonian, anticonvulant, cytostatic, antinflammatory, antiparkingonian, anticonvulant, cytostatic, antinflammatory, antidabetic, immunosuppressive, anti-HIV.

Comprision antibacterial and antiparasitic. Peptides of the invention are useful for treating comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune constraint reperfusion injury), immune diseases (e.g. autoimmune constraint reperfusion injury), immune diseases (e.g. autoimmune constraint lugus erythematosus, diabetes melliturs, pernicious andemia), myelodegenerative diseases, viral diseases, viral diseases, viral diseases, und degenerative diseases, viral diseases, und degenerative diseases, und diseases, und diseases, und diseases, und diseases, und degeneration, cataracts, crohn's diseases, uncertaive colitis, cataracts, pancreatitis, infectious diseases including bacteria, parasite, prion-based diseases, and decelerated aging. The current sequence represents a streptokinase condering derived peptide of the invention with an ability to ameliorate cell
                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; hypothermia; brain; spinal cord; kidney; heart; lung; llver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzhelmer's disease; familial amyotrophic lateral sclerosas; atherosclerosis; heart failure; infarction; heart disease; crebellar degeneration; cardiovascular disease; infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; pernicious anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides; Megener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;
                                                                                                                                                                            New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 23; Length 16; 100.0%; Pred. No. 1.9; o; Mismatches 0; Indels
                       (MOLE-) MOLECULAR THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY25013 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                   Claim 7; Column 5; 18pp; English.
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Best Local Similarity 100..
                                                                                                                            WPI; 2002-266542/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AA;
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                                                                          Krystal G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;

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melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cararact; pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline.
                                                                                                                                                                                           Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation
                                                                                                       96US-0759599.
                                                                                                                      95US-0008233.
96US-0759599.
                                                                                                                                                              Krystal G, Rabkin SW;
                                                                                                                                                                              WPI; 1999-394231/33.
                                                                                                                                              (RABK/) RABKIN S W.
                                                                                                       05-DEC-1996;
                                                                                                                       06-DEC-1995;
05-DEC-1996;
                                                                        US5917013-A.
                                                                                        29-JUN-1999.
                                                         Synthetic.
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Claim 6; Column 12; 15pp; English.

ANY SEGONS AT ANY SEGONS ARE NOVED PREDICTED BY CONTROL OF THE PRODUCTS of the invention and their encoding ameliorate cell death. The products of the invention and their encoding runcles acids may be useful for treating diseases and conditions related to aging, cellular differentiation, physical insult (e.g. physical and trauma, anoxia, hyperthermia, hypothermia, chemically induced damage, and trauma to the brain, spinal corders (e.g. hepatitis, retroviral and any other organ), viral disorders (e.g. hepatitis, retroviral infections, viral encephalitis, and AIDS/HIV), neurodegenerative disease, cerebellar degenerations, and familial amyotrophic lateral scalerosis (FALS)), cardiovascular disease, Alzheimer's disease, retroviral scalerosis (FALS), cardiovascular disease, antherosclerosis, corpertusion injury, and hypertenate disease (e.g. atherosclerosis, corpertusion injury, and hypertenate disease), immune disease (e.g. arberosclerosis) arbettes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema cordesum, Sjognen's systemic lupus erythematosus, insulin-dependent, degener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome, Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome, wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome, breast, brain, colon, cervix, and prostate, Hodgkin's lupus, arcithomas, methomas, melanoma, cancers of the sarcomas, myelomas, arcithomas, menomas, melanoma, cancers of the corder organs, ischemia or reperfusion injury, renal ischemia or infarction, and stroke, toxic insult (e.g. luver toxicity, pulmonary toxicity, toxic damage to other corgans from chemicals, radiation, and other novious substances), macular chemicals, accelerated aginal cord issease (e.g. mycoracial incordines, accelerated aginal cord issease (e.g. mycoracial incordines, and demyclinating disease), bypass surgery, chemically, chemically, chemically, chemically, pulmonary conticity of and anthracyclines.

and anthracyclines.

18 AA;

Gaps ö 100.0%; Score 30; DB 20; Length 18; 100.0%; Pred. No. 2.2; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100... Gi Conservative

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SVDVEY
           SVDVEY
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KA Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; KA cellular differentiation; physical insult; trauma; anoxia; hyperthermia; hyporthermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; nutral disorder; hepatitis; retroviral; infection; encephalitis; FALS; hutington's disease; Alzheimer's disease; Huntington's disease; Alzheimer's disease; KW familial amyotrophic lateral sclerosis; sheart failure; KW familial amyotrophic lateral sclerosis; atherosalerosis; heart failure; KW infarction; heart disease; rheumatoid arthritis; renal; retinal; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lugus erythematosus; insulin-dependent; diabetes mellitus; systemic lugus erythematosus; insulin-dependent; diabetes mellitus; systemic lugus erythematosus; insulinis; anti-phospholipid syndrome; bogren's syndrome; temporal arthritis; autoimmune polyarthritides; heuroma; melanoma; cancer; betast; colon; corvix; prostate; Hoddkin's disease; kW pancreatitis, Crohn's disease; kW pancreatitis, Crohn's disease; lowen's disease; calvillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline.
                                                                                                                    Streptokinase derived peptide 6 for amelioration of cell death.
                             AAY25014 standard; peptide; 20 AA.
                                                                                        (first entry)
                                                                                        23-AUG-1999
                                                           AAY25014;
RESULT 5
              AAY25014
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Synthetic.

US5917013-A.

29-JUN-1999.

96US-0759599. S-DEC-1996;

96US-0759599. 95US-0008233. 06-DEC-1995; 05-DEC-1996;

RABK/) RABKIN S W.

Krystal G, Rabkin SW;

WPI; 1999-394231/33.

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 7; Column 12; 15pp; English.

AMY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

nucleic acids may be useful for treating diseases and conditions related

to aging, cellular differentiation, physical insult (e.g. physical

trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

and any other organ), viral disorders (e.g. hepatitis, retroviral

infections, viral encephalitis, and AIDS/HIV), neurodegenerative

disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's

disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's

clerosis (FALS)), cardiovascular disease (e.g. atherosclerosis

myocardial infarction, heart failure, cardiomyopathy, myocardial

repertualson injury, and hypertensive heart disease), immune disease (e.g.

repertualson injury, and hypertensive heart disease), immune disease (e.g.

repertualson injury, and hypertensive heart disease), immune disease (e.g.

repertualson injury, and hypertensive heart disease), immune disease (e.g.

repertualson injury, and hypertensive heart disease), immune disease (e.g.

repertualson systemic lupus servicious anaemia, dermatomyositis, enythema

nodosum, Sjogren's syndrome, temporal archritis, myasthenia gravis,

Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,

and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,

sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the

Claim 8; Column 5; 18pp; English.

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breast, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxicus substances), macular degeneration, cataract formation, and other noxicus substances), macular ulcerative collisis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord disease (e.g. motor and demyelinating disease), bypass surgery, chemotherapy,
                                                                                                                                                                                                                                                                                                                                                              and anthracyclines
             888888888888888888888
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20 AA; Sequence

Gaps · 0 100.0%; Score 30; DB 20; Length 20; 100.0%; Pred. No. 2.4; 0; Indels 0; Mismatches 6; Conservative Query Match Best Local Similarity 1 SVDVEY 6 SVDVEY Matches ઠે 음

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RESULT 6 **ABB**80006

ABB80006 standard; peptide; 20 AA.

ABB80006;

(first entry) 26-JUL-2002

Streptokinase derived peptide#6.

Streptokinase; cell death, apoptosis; necrosis; nootropic;
mutinflammatory; antidarkinsonian; anticonvulsant; cytostatic;
mutinflammatory; antidarkintic; antichnematic; cardiant;
mutinflammatory; antidarkintic; antichnematic; cardiant;
mutinloer; antidacterial; antidacerial; antidacerial; antidacerial; antidacerial; antidacerial; antidacerial; antidacerial; antidacerial;
mutinloer; antidacerial; antidacerial; or eurodegenerative disease;
my Parkineon; s disease; Alzheimer's disease; Huntington's disease;
my cerebellar degeneration; neoplastic disease; Huntington's disease;
my cardial reperfusion; neoplastic disease; autoimmune disease;
myocardial reperfusion injury; immune disease; autoimmune disease;
myocardial reperfusion injury; immune disease; autoimmune disease;
myocardial reperfusion injury; immune disease; autoimmune disease;
myelodegenerative diseases; diadetes mellitus; pernicious anaemia;
myelodegenerative diseases; ulcerative colitis; pancreatiis; prion disease; aging

Synthetic.

US6348567-B1

19-FEB-2002.

19-APR-1999;

99US-0294457

95US-008233P. 06-DEC-1995; 05-DEC-1996; (MOLE-) MOLECULAR THERAPEUTICS INC.

Rabkin SW; Krystal G,

WPI; 2002-266542/31.

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antiparkinsonian, anticonvulsant, cytostatic, antibacteries anticonvulsant, cardiant, cantidiabetic, antianaemic, virucide, ophthalmological, dermatological, antidiabetic, antianaemic, virucide, ophthalmological, comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including conneur diseases (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases, acquired immunodeficiency syndrome (AIDS), rheumatorid arthritis, systemic lupus erythematosus, diabetes mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases, of converse including bacteria, parasite, prion-based diseases, and deseases, understative colitis, cataracts, pancerative diseases, accelerated aging. The current sequence represents a streptokinase colling anaemiah, in rawiar myelome with an ability to amellorate cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       death in cardiac myocytes
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20 AA; Sequence

Gaps . 0 'Match 100.0%; Score 30; DB 23; Length 20; Local Similarity 100.0%; Pred. No. 2.4; es 6; Conservative 0; Mismatches 0; Indels Indels Query Match Best Loc Matches

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RESULT 7

ABG76052 standard; peptide; 20 AA.

ABG76052;

(first entry) 20-MAY-2003

Streptokinase fragment based, cell death ameliorating, 20mer peptide.

Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atherosclerosis; myocardial infarction; immune disease; cardinoma; rheumatoid arthritis; myocardial infarction; immune disease; cardinoma; arthritis; inflammatory disorder; arthritis; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; physical insult; severe shock; ischaemia; reperfusion injury; cell death associated procedure; spinal cord reperfusion injury; toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease; demotherapy; viral disease; viral encephalitis; infectious disease; bacterial disease; prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging; oxidative stress.

Synthetic.

JS2002165129-A1.

07-NOV-2002.

31-JUL-2001;

95US-008233P. 99US-0294457. 06-DEC-1995; 19-APR-1999;

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The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliozating cell death, its derivative or analogue, comprising a sequence val-Asp-Val, where the peptide is in a suitable pharmaceutical camposition.

Comprising the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's disease and Alzheimer's disease; cardiovaccular disease e.g. AIDS and therosclerosis and myocardial infarction; immune disease e.g. AIDS and therosclerosis and myocardial infarction; immune disease e.g. AIDS and inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and severe shock; inflammatory disorder e.g. arthritis and inflammatory induced cell capacity; spinal cord disease e.g. myocardial ischaemia and spinal cord roxicity; spinal cord disease e.g. motor neuron disease and duillain-Bare synderome; procedures associated with cell death e.g. bypass surgery and infectious disease e.g. hepatitis and viral encephalitis; infectious disease e.g. hepatitis and viral encephalitis; infectious disease e.g. hepatitis and viral encephalitis; macular degeneration; cataract formation; panoreatitis; Crohn's disease; macular degeneration; cataract formation; panoreatitis; Crohn's disease; concertive colitis; accelerated aging and oxidative stress in a warm-blooded animal. The present sequence represents the amino acid sequence of a coner peptide capable of ameliorating cell death which is based on a
                                                                                                                                                                                                                                     Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 3; 19pp; English.
96US-0759599
                                                                                                                                  Krystal G, Rabkin SW
                                                                                                                                                                                      WPI; 2003-246673/25
                                                 (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
05-DEC-1996;
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20 AA; Sequence

Gaps .. 100.0%; Score 30; DB 24; Length 20; 100.0%; Pred. No. 2.4; cive 0; Mismatches 0; Indels 6; Conservative Best Local Similarity Query Match Matches

SVDVEY 6 1 SVDVEY 6

AAY25015 standard; peptide; 21 AA

AAY25015;

23-AUG-1999 (first entry)

Streptokinase derived peptide 7 for amelioration of cell death.

Streptokinase; cell death; amelioration; treatment; disease; aging; AlDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; bypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; huntington's disease; cerebellar degeneration; cardiovascular disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; innoventalin-dependent, diabetes mellitus; pernicious anaemia; dermatomyopathy; hypertensive; myosatial; systemic lupus erythematosus; innulin-dependent, diabetes mellitus; pernicious anaemia; dermatomyopathy; encosumune polyarthritides; Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides; wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;

melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;

Synthetic.

US5917013-A.

29-JUN-1999

96US-0759599 05-DEC-1996;

95US-0008233. 96US-0759599. 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Krystal G, Rabkin SW;

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 8; Column 12; 15pp; English

ANY 25009-Y25019 are novel peptides derived from streptokinase that ameliorate cell death. The products of the invention and their encoding or nucleic acids may be useful for treating diseases and conditions related to aging, cellular differentiation, physical insult (e.g. physical cord trauma, anoxia, hyperthermia, hypothermia, chemically induced damage, and trauma to the brain, spinal cord, kidey, heart, lungs, liver, skin and trauma to the brain, spinal cord, kidey, heart, lungs, liver, skin cord cand reman to the brain, spinal cord, kidey, heart, lungs, liver, skin and any other organ), viral disorders (e.g. hepatitis, retroviral cord cand envised to the parkinson's disease, Alzheimer's disease, lungs, liver, skin cardiovascular disease (e.g. atherosclerosis, mycardial infarction, heart failure, cardiowypathy, mycoardial cord cardiovascular disease (e.g. atherosclerosis, mycardial infarction, heart failure, cardiowypathy, mycardial infarction, heart failure, cardiowypathy, mycardial infarction, heart failure, cardiomypathy, mycardial cardiomypathy, benicked architis, systemic lupus erythematosus, inmune disease (e.g. atherosclerosis, repertusion injury, and hypertensive heart disease), immune disease (e.g. and autoimmune polyarthitides), a meoplastic disorder (e.g. lether and and autoimmune polyarthitides), a meoplastic disorder (e.g. lether and and autoimmune polyarthitides), an emplastic disorder (e.g. inflammatory disorders and inflammatory disorders (e.g. inflammatory into cher or the ordivin's lymphoma), inflammatory disorders (e.g. inflammatory into cher or reperfusion injury, retail ischemia, spinal cord ischemia and cordines, reperfusion injury, retail ischemia, spinal cord ischemia and cordina, and stroke), toxic insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other corgans from chemicals, replant or infarction, and stroke), toxic insulting disease, degeneration, cataract formation, and other noxious substances), and demyelinating disease, by any and therapeutics such as closaphine

21 AA; Sequence

Gaps .. 0 Length 21; 0; Indels 100.0%; Score 30; DB 20; Similarity 100.0%; Pred. No. 2.6; 6; Conservative 0; Mismatches 0; Local Similarity Query Match Matches

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1 SVDVEY 6

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SVDVEY

accelerated aging. The current sequence represents a streptokinase derived peptide of the invention with an ability to ameliorate cell death in cardiac myocytes.

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Gaps

.; 0

DB 23; Length 21; 2.6; 0; Indels

Score 30; DB Pred. No. 2.6; y Mismatches

100.08;

Local Similarity 100. nes 6; Conservative

Best Loca Matches

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21

Sequence

888888

Query Match

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1 SVDVEY 6

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neuroprotective; antiparkinsonian; anticonvulsant; cytostatic; antianflammatory; antiarthritic; antirheumatic; cardiant; antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV; dermatological; antidabetic; antianammics virucide; ophthalmological; antibacterial; antiparasitic; neurodegenerative disease; parkinson's disease; antinagron's disease; cereballar degeneration; neoplastic disorder; cancer; inflammatory disorder; arthritis; inflammatory joint disorders; antialmoscalellar disease; heart failure; atherosclerosis; myocardial reperfusion injury; immune disease; autoimmune disease; acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
                                                                                                                                                                                                                                                                                                 systemic lupus erythematosus; diabetes mellitus; pernicious anaemia; myelodegenerative diseases; viral diseases; macular degeneration; cataract; Crohn's disease; ulcerative colitis; pancreatitis;
                                                                                                                                    Streptokinase; cell death; apoptosis; necrosis; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR THERAPEUTICS INC.
                            ABB80007 standard; peptide; 21 AA
                                                                                                         Streptokinase derived peptide#7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-008233P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0759599
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krystal G, Rabkin SW;
                                                                                                                                                                                                                                                                                                                                              prion disease; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-266542/31.
                                                                                                                                                                                                                                                                                                                                                                                                  US6348567-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1995;
                                                                                26-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                           9-FEB-2002
                                                     ABB80007;
RESULT 9
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Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis, rheumatic fever.

Streptococcus equisimilis.

WO9908698-A1.

25-FEB-1999

98WO-US17114. 97US-0055911

18-AUG-1998; 18-AUG-1997; GEHO) GEN HOSPITAL CORP

HARVARD COLLEGE

HARD

Reed

Parhami-Seren B,

WPI; 1999-190113/16.

Claim 9; Column 5; 18pp; English

Antigenic epitope of streptokinase, spanning amino acids 138-208

(first entry)

18-JUN-1999

AAY01550,

AAY01550 standard; peptide; 71 AA.

AAY01550

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (PI) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. Pl is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an antigenic epitope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 20;
100.0%; Pred. No. 10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 5; 44pp; English
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Best Local Similarity
Local 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of cor its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antiatherosalerotic, vasokropic, immunosuppressive, anti-HTV.

C antinflammatory, antidiabetic, antianeamic, virucide, ophthalmological, dermatological, antidiabetic, antianeamic, virucide, ophthalmological, antiulcates apoptosis and necrosis in a warm-blooded animal. Compositions comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's comprising peptides of the invention are useful for treating cancer, inflammatory disorders (e.g. Parkinson's, Alzheimer's, Huntington's disorders in carcinson injury), immune diseases (e.g. authritis, inflammatory joint disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis, systemic lupus erythematosus, diabetes mellitus, permicious anaemia), systemic lupus erythematosus, diabetes mellitus, permicious anaemia), wysloegenerative diseases, ustanaemia, any organ. Other disorders include macular degeneration, cataracts, and essess and cromanaemia), any organ. Other disorders include macular degeneration, cataracts, and testive solicis, parasite, prion-based diseases, and
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RESULT 11 AAY01558

Tue Jan

AAY01558,

25-FEB-1999.

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induces fibrin-dependent plasmingen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of anno acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a mucleic acid (1) encoding a modified bacterial streptokinase protein; the expression vector comprising (1) and (4) a host cell transformed with the expression vector comprising (1), and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a become plasmingen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proceolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold, The present represents recombinant streptokinase, designated rSK144-293.
                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated bacterial protein that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide corresponding to amino acids 120-352 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 30; DB 20; Length 150; 100.0%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                          Claim 34; Page 67-68; 73pp; English.
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                                                                                                                                                                                                                                                                                                                 N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                  98WO-US26694
                                                                                                           97US-0069497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                      (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                             WPI; 1999-395183/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 AA;
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                                                                                                                                                                                                                                                                    N-PSDB; AAX80494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatic fever
                                                                  15-DEC-1998;
                                                                                                           15-DEC-1997;
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                         24-JUN-1999
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                                                                                                                                                                                                 Reed GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a peptide corresponding to amino acids 148-293 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (PI) comprising an epitope which activity of streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. It is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus, streptokinase, fibrin-dependent plasminogen activator, nSK; rSK; bacterial; blood clot, thrombotic condition, myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                      ptide, streptokinase, streptokinase-specific antibody, activity, thrombolytic therapy, glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                             Peptide corresponding to amino acids 148-293 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 30; DB 20; Length 146; 100.0%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 13, 44pp, English.
AAY01558 standard; peptide; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY24796 standard; Protein; 150 AA
                                                                                                                                                                                                                                                                                                                                                                                               98WO-US17114.
                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0055911
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                                                                                  (first entry
                                                                                                                                                                                                                                                                 Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-190113/16.
                                                                                                                                                                        peptide;
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                                                                                                                                                                                                                        rheumatic fever.
                                                                                                                                                                                               thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1998;
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                                                                                    18-JUN-1999
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Sequence

Query Match

Matches

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AAY24796;

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Gaps

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0; Indels

Gaps

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Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and Arg 45 to Gly 68 also being deleted. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity.

The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction.

See also AAQ10230, AAR10195 and AAR10197-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high purity prodn
                                                                              16; Length 297;
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                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic gene encoding streptokinase - scale, of streptokinase used as a thrombolytic agent
                                                                          100.0%; Score 30; DB 100.0%; Pred. No. 52;
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Streptokinase (1-372, 45-68 deficient)
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                                                                                                                                                                                                                                                                          AAR10196 standard; Protein; 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SAKA ) OTSUKA PHARM FACTOR
                                                                                                               6; Conservative
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                                                                                                                                                                                   183 SVDVEY 188
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                                                                                           Best Local Similarity
Matches 6; Conserv
                                         297 AA;
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11-JUL-1989;
27-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                       Sequence
                                                                                                                                                                                                                                                                                                              AAR10196;
                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY24795
                                                                                                                                                                                                                                         RESULT 15
AAR10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
AAY24795
ID AAY24'
XX
AC AAY24'
                                                                                                                                                                                                                                                                                             %XGXGCCCCCX8XTXBXBXBXBXBXBXBXBXBXBXBXBXBXBXBXBX
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                                                                                                                                                                                   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                              The present sequence represents a peptide corresponding to amino acids 120-352 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. In is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of streptokinase encoded by a pST-1 HindIII fragment. Recombinant streptokinase can be produced by culturing bacteria transformed with a high efficiency plasmid contg. the streptokinase gene, amplified by using haemolytic Streptococcus as the template and using inducers based on the streptokinase nucleotide sequence. The recombinant streptokinase is used to treat thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  streptokinase; recombinant production; haemolytic Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prepn. of streptokinase - useful for treating thrombus diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                       New polypeptides which bind streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 20; Length 233; 100.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR91599 standard; Protein; 297 AA.;
                                                                                                                                                                                                               Disclosure; Page 13; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese
                                                                                                                                                                             useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYSH-) UNIV SHANGHAI MEDICAL
97US-0055911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-CN00024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94CN-0112106
                                                                                     Parhami-Seren B, Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 6-8; 24pp;
                               (GEHO ) GEN HOSPITAL CORP.
(HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                         WPI; 1999-190113/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-358628/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 SVDVEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT29961
18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9527050-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91599;
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RESULT 14

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Gaps

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Song H;

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The sequence was deduced from DNA obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642.

ATCC 9642.

Minal and engineered to add a Met codon prior to codon 16 of the streptokinase CDS. The construct was used to prepare expression vector pGG06 for prodh. of the streptokinase core molecule.

See also AARL2887-R12889, AARL2891-R12893, AARL2885 and AARL3522. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                         Fusion protein, blood clotting, coagulation, fibrinolysis, antithrombotic, thrombolysis, streptokinase, thrombin.
                                                                                                       Streptococcus equisimilis ATCC 9542 or ATCC 10009
                                                                                                                                                                    2..369
/label= core streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 88; 115pp; English.
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                              /note= "AAs 16-383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRBI-) BRITISH BIO-TECHNOLOGY LTD.
  Truncated Met streptokinase.
                                                                                                                                                                                                                                                                                                                                           90WO-GB01911.
                                                                                                                                                                                                                                                                                                                                                                                     90WO-GB01911
                                                                                                                                                                                                                                                                                                                                                                                                        89GB-0027722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-208151/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ12159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SVDVEY
                                                                                                                                                                                                                                                                                                                                           07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1989;
                                                                                                                                                                                                                                                     409109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-1991
                                                                                                                                                                                                                                                                                                 27-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP407942-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR10195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR10195
  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         induces fibrin-dependent plasmingen activation in a pharmaceutical composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a modified treptokinase in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a multiple carification to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; the expression vector comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for a bacterial fibrin-dependent plasminogen activator is useful for myocardial infarction, venous thrombosis. pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least on amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence represents recombinant streptokinase designated rSK59-414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                               Streptococcus, streptokinase, fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated bacterial protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 30; DB 20; Length 356; 100.0%; Pred. No. 64; ive 0; Mismatches 0; Indels
                                         Recombinant streptokinase rSK59-414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 35; Page 65-66; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR12892 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                         98WO-US26694
                                                                                                                                                                                                                                                                                                                                                                                97US-0069497
(first entry)
                                                                                                                                                                                        Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-395183/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 SVDVEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX80493
                                                                                                                                                                                                                                                                                                                                         15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1997;
26-AUG-1999
                                                                                                                                                                                                                                                     WO9931247-A1
                                                                                                                                                                                                                                                                                             24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
17-SEP-1991
                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR12892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed GL;
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                                Gaps
                                0
 DB 12; Length 369;
                                Indela
                                                                                                                                                                                                                                                                                                              streptokinase; thrombolytic agent; myocardial infarction.
                                .
0
100.0%; Score 30; DB 100.0%; Pred. No. 67;
                                Mismatches
                                                                                                                                                                                                                                                                              Streptokinase (1-372, Phe 118 deleted).
                                                                                                                                                                               AAR10195 standard; Protein; 371 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              90EP-0113099
                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1990;
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Matches

ઠે d RESULT 17 AAR1289

AXAXEEX XEEXX

Gaps

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Indels

Length 372;

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256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-6 and AAR10198-R10200.
                                                                                                                                                                                                                                                                                      streptokinase; thrombolytic agent; myocardial infarction
                                                                                                        ô
                                                                                  , DB 12;
, 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venoyama
                                                                                                        0; Mismatches
                                                                                  100.0%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakata Y,
                                                                                                                                                                                                   AAR10200 standard; Protein; 372 AA.
                                                                                                                                                                                                                                                                Streptokinase (1-372) derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 59; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                            90JP-0096830.
89JP-0179432.
89JP-0307957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ono K,
                                                                                                                                                                                                                                                                                                                                                                       90EP-0113099.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                                                                                                                             (first entry)
                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogino K,
                                                                                                                                               157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-016179/03
                                                                                  Query Match
Best Local Similarity
                                                              372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                            1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1990;
11-JUL-1989;
27-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1990;
                                                                                                                                                                                                                                            28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                  16-JAN-1991
                                                                                                                                                                                                                                                                                                                             BP407942-A.
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Мајіша Е,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                               Sequence
                                                                                                                                                                                                                        AAR10200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                              RESULT 20
AAR10200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                        Matches
  888888
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                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Ly8 414) and Phe at position 118 being deleted. Alternatively, Phe 118 can be replaced with any other amino acid. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230 and AAR10196-R10200.
                                                                                                                high purity prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and Gln being substituted for Lys at both positions
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                    Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptokinase; thrombolytic agent; myocardial infaction.
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  high
                                                                                                                                                                                                                                                                                                       o;
                                                                        Uenoyama
                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 12; 100.0%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uenoyama
                                                                                                                Synthetic gene encoding streptokinase - scale, of streptokinase used as a thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scale,
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic gene encoding streptokinase - of streptokinase used as a thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptokinase (1-372, Gln 256, Gln 257)
                                                                       Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                    AAR10197 standard; Protein; 372 AA
                                                                                                                                               Claim 8; Page 59; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90JP-0096830.
89JP-0179432.
89JP-0307957.
        90JP-0096830.
89JP-0179432.
89JP-0307957.
                                                                       Ono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ono K,
                                                  (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90EP-0113099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                            Local Similarity 100
es 6; Conservative
                                                                       Ogino K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogino K,
                                                                                           WPI; 1991-016179/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-016179/03
                                                                                                                                                                                                                                                                                                                                                156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                            SVDVEY 6
                                                                                                                                                                                                                                                               371 AA
         11-APR-1990;
11-JUL-1989;
27-NOV~1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-1990;
11-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-1991
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP407942-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Majima E,
                                                                       Мајіта Е,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        AAR10197
                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                           Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lyg 414) and retaining streptokinase activity. One or more of the amino acids can be replaced by a different amino acid at the same position or it can be deleted Alternatively, an extra residue can be inserted into the sequence. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in platients with lung thrombus or myocardial infarction. See also AAQ10230 and AAR10195-R10199.
Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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100.0%; Pred. No. 68;
iive 0; Mismatches 0;
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Forrens Madrazo IDC, Garcia Ojalvo A,
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Streptococcus
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                                                                                                                   11-APR-1990;
                                                                                                                                        27-NOV-1989;
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                                                                          16-JAN-1991
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                                                   EP407942-A.
                               Synthetic.
                                                                                                                                                                                   Мајіта Е,
                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                    Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the Nor C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a mutant protein of the streptokinase SKC-2. Streptokinase forms a complex with plasminogen, activating its conversation to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full-length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
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                                                                                                                                                                                                                                                                                                   Garcia Ojalvo A, De La Fuente Garcia JDJ;
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                                                                                                                 Streptokinase, SKC-2; plasminogen, plasmin; antigenicity, plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
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                                                                                              Amino acid sequence of a mutant streptokinase.
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                               AAY84006 standard; Protein; 372 AA
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                                                                        (first entry)
                                                                                                                                                                        Streptococcus equisimilis.
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Seralena Menendez A;
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                                                                        03-JUL-2000
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                                                   AAY84006;
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AAR10198
ID AAR10
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DT 28-MA
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DT 28-MA
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           RESULT 21
                   AAY84006
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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streptokinase; thrombolytic agent; myocardial infarction.
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89JP-0179432.
89JP-0307957.
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                                                                                                                                                                                                                                                                                                                                                                        (SAKA ) OTSUKA PHARM FACTOR
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Best Local Similarity 100.
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De La Fuente Garcia JDJ;

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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the Nor C-terminus -
                                                                                                                                                                  The present sequence represents a mutant protein of the streptokinase SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigonicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full-length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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                                                                                                                                          Disclosure; Page 24-25; 54pp; English
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89JP-0179432.
89JP-0307957.
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Seralena Menendez A,
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                              2000-226041/20
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N-PSDB; AAZ99252
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11-JUL-1989;
27-NOV-1989;
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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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example of a streptokinase derivative which is a combination of two individually claimed modifications. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-8 and AAR10200.
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                      Length 391;
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                                                                                                                                                                      100.0%; Score 30; DB 12; 100.0%; Pred. No. 72;
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                                                                                                                                       391 AA;
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Length 401;

DB 21;

100.0%; Score 30;

Query Match

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We streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; We cellular differentiation; physical insult; trauma; anoxia; hyperthermia; whypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; wiral disorder; hepatitis; retroviral; infection; encephalitis; FALS; merrodegenerative disorder; Parkinson's disease; Alazieimer's disease; Muttington's disease; cerebellar degeneration; cardiovascular disease; Muttington's disease; cardiownowopathy; hypertenaive; morardial; minance disease; rheumatodid arthritis; renal; retinal; we perfusion injury; immune disease; rheumatodid arthritis; renal; retinal; we perfusion injury; immune disease; rheumatodid arthritis; renal; retinal; we syndrome; temporal arthritis; autoimmune polyarthritides; pernicious anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; syndrome; temporal arthritis; autoimmune polyarthritides; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's Lymphoma; inflammatory disorder; stroke; ischemia; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's Lymphoma; inflammatory disorder; stroke; ischemia; we beinal cord; toxic insult; pulmonary; macular degeneration; cataract; appinal cord; toxic insult; pulmonary; moral adgeneration; cataract; cherching and disease; bypass surgery; contains and disease; bypass surgery;
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                                                                    Gaps
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                          Pred. No. 74;
; Mismatches
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0008233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                    6; Conservative
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                                                                                                                                                                                                          144 SVDVEY 149
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                              Best Local Similarity
                                                                                                                                     1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5917013-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY25020;
                                                                    Matches
                                                                                                                                                                                                                                                                                                                        RESULT 26
AAY25,020
AAY25,
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cheumatoid arthritis, systemic lupus erythematoeus, insulin-dependent, diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema nodosum, Sjogran's syndrome, temporal arthritis, mari-phospholipid syndrome, modosum, Sjogran's syndrome, temporal arthritis, anti-phospholipid syndrome, and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia, sarcinomas, melanoma, cancers of the beast, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or repertusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia or infarction, and stroke), toxic reperfusion injury, retinal ischemia or infarction, and stroke), toxic cangans from chemicals, radiation, and other noxicity, toxic damage to other organs from chemicals, radiation, and other noxicity, toxic damage to other cargans from chemicals, radiation, and other noxicity, spinal cord disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and empelinating disease), bypass surgery, chemicherapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                    chemically-induced reperfusion, and therapeutics such as clozapine, AZT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
reperfusion injury, and hypertensive heart disease), immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia Ojalvo A, De La Fuente Garcia JDJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptokinase, SKC-2; plasminogen; plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 30; DB 20; Best Local Similarity 100.0%; Pred. No. 76; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 20-21; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84005 standard; Protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98CU-0000119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torrens Madrazo IDC,
Seralena Menendez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-226041/20
                                                                                                                                                                                                                                                                                                                                                                                                           and anthracyclines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ99250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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the present sequence represents a mutant protein of the streptokinase

The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulant, cytostatic, antiparkinsonian, anticonvulant, cytostatic, antiantherosalerotic, vasotropic, immunosuppressive, anti-HTV.

CC antialherosalerotic, vasotropic, immunosuppressive, anti-HTV.

CC dermatological, antidiabetic, antiparasitic. Peptides of the invention are useful for treating comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. harthritis) inflammatory disorders including cancer, inflammatory disorders (e.g. arthritis) inflammatory joint diseases and cerebellar diseases (e.g. heart failure, atherosalerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases, acquired immunodeficiency syndrome (ALDS), rheumatorial arthritis, systemic lupus erythematosus, diabetes mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases, viral diseases, and degenerative diseases, undertaive colitis, cataractes, panceraitis, infectious diseases including bacteria, parasite, prion-based diseases, and errentative degenerative systemic serythematosus, darbet expensents a representative

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Gaps

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0; Indels

0; Mismatches

Query Match
Best Local Similarity 100.
Matches 6; Conservative

156 SVDVEY 161

1 SVDVEY 6

ò 셤 ABG74199 standard; Protein; 413 AA.

RESULT 29 ABG74199 06-MAY-2003 (first entry)

100.0%; Score 30; DB 23; Length 413; 100.0%; Pred. No. 76;

streptokinase amino acid sequence.

413 AA;

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Streptokinase; cell death, apoptosis; necrosis; nootropic;
neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;
neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;
mutiantherosclerotic; vasotropic; immunosuppressive; anti-HIV;
dermatological; antidabetic; antianaemic; virucide; ophthalmological;
wintulcer; antibacterial, antiparastic; neurodegenerative disease;
wartulcer; antibacterial, antiparastic; neurodegenerative disease;
w rebellar degeneration; neoplastic disease; Huntington's disease;
w inflammatory disease; heart failure; atherosclerosis;
w cardiovascular disease; heart failure; atherosclerosis;
w myocardial reperfusion injury; immune disease; autoimmune disease;
acquired immunodeficiency syndrome; AlDS; rheumatoid arthritis;
cyclired immunodeficiency syndrome; AlDS; rheumatoid arthritis;
w myelodegenerative diseases; viral diseases; macular degeneration;
w cateract; croh's disease; ulcerative colitis; pancreatitis;
SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infraction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                          100.0%; Score 30; DB 21; Length 413; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB80012 standard; protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase amino acid sequence.
                                                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 100.00
Best Local Similarity 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                 144 SVDVEY 149
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                                                                                                                                                                                                                         Sequence 413 AA;
                                                                                                                                                                                                                                                                                                                                 1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80012;
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80012
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Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atherosclerosis; myocardial infarction; immune disease; carctinoma; rheumatorid arthritis; meoplastic disorder; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; arthritis; inflammatory induced cell damage; motor neuron disease; cell dath associated procedure; spinal cord creperfusion injury; toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease; toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease; chemotherapy; viral disease; bypass surgery; myocardial ischaemia; chemotherapy; viral disease; viral encephalitis; infectious disease; bacterial disease; princeatitis; Crohn's disease; ulceration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156..171
/label= 18mer_peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2. This is SEQ ID NO 5 as shown
in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Cell death ameliorating peptide. Specifically claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
156..161
/label= 6mer_peptide_#1
/note= "Cell death amel:
                                                                                                           Representative streptokinase sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              accelerated aging; oxidative stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
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(MOLE-) MOLECULAR THERAPEUTICS INC.

Krystal G, Rabkin SW;

WPI; 2002-266542/31.

99US-0294457. 95US-008233P.

.9-APR-1999; 06-DEC-1995; 05-DEC-1996;

19-FEB-2002.

prion disease; aging

Synthetic.

Disclosure, Fig 3, 18pp, English

1 SVDVEY

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/note= "Cell death ameliorating peptide. Specifically claimed in claim 2. This is SEQ ID NO 5 as shown on page 8".
                                                                                               156..176
/label= Fraction_13_peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                                                                                                       6mer peptide #2
"Cell death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= limer peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Fraction 12 peptide
/note= "Cell deaTh ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 30; DB 24; Length 413;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           /label= 6mer_peptide
/note= "Cell death am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-008233P.
99US-0294457.
96US-0759599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS2002165129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-1999;
05-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                       Peptide
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents patients with lung thrombus or myocardial infarction. See also AAR10195-R10200.
                                                                                                                                     streptokinase; thrombolytic agent; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasminogen activator; coronary thrombosis; ATCC-9542
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0
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                                                                                                                                                                                                                                                                                                                                                                           of streptokinase used as a thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB
100.0%; Pred. No. 76;
ive 0; Mismatches
                                                                                                                 Streptokinase encoded by synthetic gene.
                                                                                                                                                                                                                                                                                                            Ono K, Sakata Y,
                                                   AAR10194 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR20202 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 51; 76pp; English.
                                                                                                                                                                                                                                             90JP-0096830.
89JP-0179432.
89JP-0307957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%;
6; Conservative C
                                                                                                                                                                                                                           90EP-0113099.
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                                                                                                                                                                                                                                                                                       (SAKA ) OTSUKA PHARM FACTOR
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                            Majima E, Ogino K,
                                                                                                                                                                                                                                                                                                                                  WPI; 1991-016179/03
156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AA;
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                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ10230
                                                                                                                                                                                                                         09-JUL-1990;
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                                                                                                                                                                                                                                                                 27-NOV-1989;
                                                                                             28-MAR-1991
                                                                                                                                                                                                                                              11-APR-1990;
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21-APR-1992
                                                                                                                                                                                                     16-JAN-1991
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                                                                                                                                                                                EP407942-A.
                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                        AAR10194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
                                          AAR10194
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Gaps

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Indels

us-09-919-703-1.open.rag

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Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                              14-414 of streptokinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 120-352 or 244-4 pref.
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB 15; Length 414; 100.0%; Pred. No. 76; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                  DNA encoding a polypeptide which binds to plasminogen and corresponds to region of streptokinase - useful to detect plasminogen in a sample and to treat myocardial infarction
                                                                                                                                                                                                                                                                                                 Nucleic acid comprising a sequence encoding amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus equisimilis native streptokinase.
                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                  Disclosure; Page 40-41; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 30; Page 60-61; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY24794 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminally deleted streptokinase
                                          92US-0956692.
             93WO-US09502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US26694
                                                                                        (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-395183/33.
                                                                                                                                                                      WPI; 1994-135561/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY 6
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             05-OCT-1993;
                                          05-OCT-1992;
29-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9931247-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY24794;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                       Reed GL;
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Matches
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                                                                                                                                                                                                                                                                                                                                            The SKC-2 gene was isolated from S.equisimilis type C by gene amplification from the synthetic primers SK1, SK2 and SK3 (see AAQ20666-8). The SKC-2 gene was inserted into yeast expression vector pPS-7 for extracellular expression of streptokinase and into pNAO for intracellular expression in yeast. For expression in bacteria, the SKC-2 gene was inserted in plasmid pEKG3, between a trp promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                              Streptokinase C-2 gene from S.equisimilis type C - plasmids and transformants for large scale intra- and extracellular expression of SKC-2 useful in thrombolytic agents
                                                                                                                                       Hidalgo AP, Doce RS, Marrero LFH;
Munoz EAM, Martinez WB, Somavilla MC;
Martinez LSH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 30; DB 13; Length 414; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptokinase; SK; Streptococcus equisimilis; plasminogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                       (INGG-) CENT ING GENETICA & BIOTECNOLOGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "claim 1, see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    see CC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR63120 standard; protein; 414 AA.
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244..414
/note= "claim 3,
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                                                                                                                                                                                                                                                                                                                 Claim 13; Page 14; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "claim 2,
                                             91AU-0078101
                                                                           90CU-0000090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Query Match
Best Local Similarity 100.vv
6; Conservative
                                                                                                                                       Chaplen RR,
Ramirez AC,
P, Garcia J,
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16-NOV-1994' (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14..414
/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myocardial infarction.
                                                                                                                                                                                                    WPI; 1992-024716/04.
N-PSDB; AAQ20665.
                                                                                                                                                                                                                                                                                                                                                                                                                                              and a T4 terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVDVEY 6
                                                                                                                                                                        Fernandez AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase
                                            31-MAY-1991;
                                                                                                                                       Garcia MPE,
                                                                            23-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9407992-A1
              28-NOV-1991
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                                                                                                                                                      Collazo PR,
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RESULT 32

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Gaps

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describes a synthetic polypeptide (PI) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. PI is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic

414 AA

Sequence

888888

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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising can mucleic acid (1) encoding a modified bacterial streptokinase; (3) an a mucleic acid (1) encoding a modified bacterial streptokinase; (3) an a mucleic acid (1) encoding a modified bacterial streptokinase; (3) and expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising (2) and (3) and (4) a host cell transformed with the expression vector of (3). The pharmaceutical condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase con also be used in non-human mammals. Streptokinase con also be used in non-human mammals. Streptokinase has at least to lefold, preferably 100-fold cancelided streptokinase has at least to ne amino acid substitution that in a mativaled streptokinase at least to sequence represents native streptokinase at least to sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigenic peptide; streptokinase; streptokinase-specific antibody;
thrombolytic activity; thrombolytic therapy; glomerulonephritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides which bind streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a native streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Native streptokinase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 12; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY01556 standard; peptide; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US17114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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SVDVEY 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatic fever.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                Gaps
                                                                                                                                                                                                                                                                                                     Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic; plasma clot, hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant streptokinase polypeptide - useful as plasmin-resistant
100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76;
                                Indels
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                                                                                                                                                                                                                                                                         Streptococcus equisimilis native streptokinase.
                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                            AAW94664 standard; Protein; 414 AA.
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                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                      fibrinolysis; resistance.
                                  6; Conservative
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                                                                                               157 SVDVEY 162
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombolytic agent
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                                                                 1 SVDVEY 6
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                                                                                                                                                                                                           AAW94664;
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                               Gapa
                                                                                                                                                                                                                                                                                    Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic; plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
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Length 414;
                               Indela
                                                                                                                                                                                                                                                        Streptococcus equisimilis mutant streptokinase K59E.
 DB 20;
100.0%; Score 30; DB
100.0%; Pred. No. 76;
ive 0; Mismatches
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14
                                                                                                                                                                    AAW94665 standard; Protein; 414 AA.
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                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                     Fibrinolysis; resistance.
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Matches 6; Conservative
                                Conservative
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                                                                                           157 SVDVEY 162
               Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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    Query Match
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157 SVDVEY 162

1 SVDVEY 6

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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein, (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species, and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune or system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.
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                                                                                                                                   Non-immunogenic, epitope, T-cell, immunogenicity; immune system; SK; immunogl bulin; therapeutic; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; cive 0; Mismatches 0; Indels 0
                                                                                                        Streptokinase (SK) protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW86144 standard; Protein; 414 AA.
            AAW86143 standard; Protein; 414 AA.
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                                                                                                                                                                                                                                                                                                         98GB-0007751.
97GB-0010480.
97GB-0016197.
97GB-0025270.
97US-0067235.
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                                                                                                                                                                                    Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (BIOV-) BIOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVDVEY 6
                                                                                                                                                                                                                                                                              21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                           28-NOV-1997;
02-DEC-1997;
                                                                                                                                                                                                                  W09852976-A1
                                                                                                                                                                                                                                                                                                                             21-MAY-1997;
                                                                                                                                                                                                                                                 26-NOV-1998
                                                                                                                                                                                                                                                                                                                                              31-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                           AAW86143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr FJ;
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AAW86144
ID AAW6
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AC AAW6
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AAW86143
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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein, (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cells epitopes) of the given species, and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of a de-immunised SK protein molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; fibronectin.
                                      Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunogl bulin; therapeutic; streptokinase; de-immunised.
                                                                                                                                                                                                                                                                                                                                                                                             proteins - by modifying the amino acid eliminate potential epitopes for T-cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 20;
100.0%; Pred. No. 76;
iive 0; Mismatches 0;
            protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 29; 77pp; English
           De-immunised streptokinase (SK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%;
les 6; Conservative C
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97GB-0016197.
97GB-0025270.
97US-0067235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. equisimilis streptokinase
                                                                                                                                                                                  98WO-GB01473
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                                                                                                                                                                                                                                                                                                                                                                                               Reducing immunogenicity of sequence of the protein to of a given species
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                                                                                       Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                       (BIOV-) BIOVATION LTD
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                                                                                                                                                                                                                              21-MAY-1997;
31-JUL-1997;
28-NOV-1997;
02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-2000
                                                                                                                     WO9852976-A1
                                                                                                                                                                                  21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                              sequence of
of a given s
                                                                                                                                                   26-NOV-1998
                                                                                                                                                                                                                4-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                     Carr FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 39
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This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between plasminogen activator (PA) comprises a polypeptide fusion between contexpokinase (SK), which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are from fibrin binding domains (PBD) 4 and 5 or 1 and 2. The hybrid PA possesses the binding domains (PBD) 4 and 5 or 1 and 2. The hybrid PA possesses the billity to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable animal or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as cardiovascular disorders. The hybrids have enhanced fibrin selectivity of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation centuation clinical use of streptokinase.
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of
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                                                                                                                                                                                     Roy C, Rajogopal K, Nihalani D, Sundaram V;
                                                                                                                                                                                                                                                                                                         Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Similarity 100.0%; Score 30; DB 21; Length 414;
6; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wild type streptokinase from Streptococcus equisimilis.
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                                                                            99EP-0310541
                                                                                                               98IN-0003825
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N-PSDB; AAA37633.
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                                                                                                                                                                                               Kumar R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 AA;
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                                                                            3-DEC-1999;
                                                                                                                   24-DEC-1998;
EP1024192-A2
                                      02-AUG-2000.
                                                                                                                                                                                             Sahni G,
Yaɗav M;
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The state of the state of the state of

Carter G;

WO200034317-A2

38-DEC-1999; 08-DEC-1998;

15-JUN-2000

02-FEB-1999;

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rectains or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for producing a protein with an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive drugs to its active form within a living organism; a vaccine, a protein used as a carrier of other molecules or a protein which binds to other molecules within or introduced within the living organism; in order to alter the collection of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a certain strains of beta-haemolytic streptoxinase is produced by certain strains of beta-haemolytic streptoxinase is produced by contract or interapeutic or a diagnostic agent. Streptoxinase is an affective thrombolytic agent in the treatment of coronary thrombosis, or improving survival and preserving left ventricular function following mycoardial infarction. The native protein is immunogenic and the protein to a single use. The new method could provide a longer corpuspentic use for streptoxinase. This is the sequence of the altered streptoxinase. The wild type streptoxinase sequence is given in AAB01295. See GENESEQ records AAB01289-B01302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
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plasmin; myocardial infarction
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99GB-0002139.
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                                                                           Streptococcus equisimilis.
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                                                                                                                                     WO200034317-A2
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                                                                                                                                                                                                                                                                                                                                   02-FEB-1999;
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AAB74940
ID AAB74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exproteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell cepitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for the producing a protein with an enzymatic activity which has a beneficial ceffect, a protein used to convert inactive drugs to its active form within a living organism, a vaccine, a protein used as a carrier of other molecule or a protein which binds to other molecules within or introduced within the living organism. The less immunogenic bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a certain strains of beta-haemolytic streptokinase is produced by certain strains of beta-haemolytic streptokinase is produced by certain strains of beta-haemolytic streptokinase is produced by promitiating its activation to plasmin and thereby promoting the continity in survival and preserving left ventricular function following organization of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, improving survival and preserving left ventricular function following convential infarction. The new method could provide a longer production of neutralising antibodies in humans generally limits the protein to a single use. The new method could provide a longer therapeutic use for streptokinase. This is the sequence of the wild type streptokinase. The altered streptokinase sequence is given in AAB01296. See GENESEQ records AB01289-801302.
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                                                                                                                                                                                                                                                                                                    Carr FJ, Adair FS, Hamilton AA, Carter G;
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                                                                                                                  99WO-GB04119
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99GB-0002139
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es 6; Conserv
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Gaps

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25-SEP-2000

AAB01296
ID AAB0
XX
XX
XX
XX
DT 25-K
XX
DE Alte
XX
KW Imm
KW vac'
KW vac'
KW pla

AAB01296;

RESULT 41

셤

Sequence

Query Match Matches RESULT 43

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Streptokinase; mutant; human; plasmin; plasminogen; thrombolytic.
Mutant streptokinase protein sequence K59E.
                                                                                            N-PSDB; AAF82144
                    Misc-difference
                                                                                   Wu H, Shr G;
                                                                 11-JUL-1995;
            Unidentified
                                                            01-JAN-2001.
                                                      TW416990-A
                                                                                                                                                                                            Seguence
                                                                                                                                                                                                 Query Match
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Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                          Streptococcus plasminogen activator, streptokinase
                                                                                                                                                                                                    Plasminogen activator, cardiant, thrombolytic;
heart attack; stroke; blood clotting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 29-31; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                       AAY99593 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  16660SD-0M66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang XC, Tang JJN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                               Streptococcus sp.
                                                                                                                                                                                                                                                                                                                         WO200032759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasminogen
                                                                                                                                                                                                                                                                                                                                                                      38-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                      AAY99593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
AAY99593
ID AAYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method to create mutants of streptokinase (SK) which become more resistant to hydrolytic inactivation by human plasmin (HPIM) and more effective in activation of chuman plasmin (HPIM) and more effective in activation of the more inactivation by human plasmin (HPIM) and more sequence of the care of a commercially available. The novel HPIM hydrolysis resistant SK can be created by the techniques of gene engineering to substitute the amino acid residues near the peptide bonds that are hydrolysed by HPIM. The mutant SK can be used to form HPIQ and native SK and could be used as a thrombolytic agent. The mutant SK sequence could be coupled with other proteins to form fusion proteins and improve the fibrinolytic activity of the fusion proteins. Some truncated SKs such as SK(16.718) could activate thing as efficiently as native SK. The truncated SKs comprising the tusion proteins activity than the corresponding native truncated SK. Since Lya59-Ser60 is among the few peptide bonds which are claaved in the early reaction with HPIM and the NH2-terminal peptide chain of the hydrolysis of the peptide bond of Lya59-Ser60 should be able to prevent the hydrolysis of the peptide bond and might improve the stability of SK as a HPIQ activator. The present sequence represents the mutant of SK as a HPIQ activator. The present sequence represents the mutant of SK as a HPIQ activator. The present sequence represents the mutant of SK as a HPIQ activator. The present sequence represents the mutant of SK as a HPIQ activator or the present invention.

N.B. The present sequence corresponds to the indexers best interpretation of the sequence given in the specification, which is of poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of novel streptokinase mutants as improved thrombolytic
                                                                                                                                                                                                                                                                             /label= unknown
/note= "given as being encoded by NNN due to poor
quality text"
                                                                                                                                                                                                         "given as being encoded by NNN due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 30; DB 22; Length 414; 100.0%; Pred. No. 76; cive 0; Mismatches 0; Indels
                                                                                                                                            'note= "Lys in wild type sequence
                                                                                                                                                                                                                                     quality text
                                                                                             Location/Qualifiers
                                                                                                                                                                                           /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1; 4pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95TW-0107238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95TW-0107238
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NASC-) NAT SCI COUNCIL
                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-326604/34.
                                                                                                                                                                                                                                                            Misc-difference 370
                                                                                                                                                                      Misc-difference 12'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 AA
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The present sequence is streptokinase, a single-peptide secretory protein which is produced by various strains of haemolytic Streptococcus. Streptokinase forms a tight binding complex with human plasminogen, causing the spontaneous conversion of plasminogen to its active form, plasmin the spontaneous conversion of plasminogen to its active form, plasmin the spontaneous conversion of plasmin ogen to its active form, plasmin the stracellular fluids of vertebrates. Plasmin is implicated in the extracellular proteolysis associated with a wide range of physiological processes. Plasminogen activators regulate plasminogen expression either by forming a binding complex, as in the case of streptokinase, or by hydrolysing a peptide bond in plasminogen activators and chymotrypsin has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful human plasminogen acid realdues 64s and 645 of full length human plasminogen acid realdues 64s and 645 of full length human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human plasminogen. Novel plasminogen activators have been made based upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the plasminogen activation/recognition site of plasminogen binding
proteins. The polypeptides are useful in preparing thrombolytic agents
for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY50870 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY50870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
AAYSO870
ID AAYSOX
XX
AC AAYSOX
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Gaps

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1 SVDVEY 6

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SVDVEY

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Streptokinase produced using E.coli transformed with a recombinant streptokinase vector can be isolated for use as a thrombolytic agent to facilitate the in vivo lysis or dissolution of blood clots. The vector is esp. a plasmid obtd. from E.coli, esp. plasmid pBR 322. Recombinant plasmid pMF1 as defined by a restriction endonuclease map is claimed. Escherichia coli HB 101 harbouring plasmid pMF1 is depositd as ATCC 39613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase A; recombinant phage; thrombolytic agent; plasminogen; plasmin.
                                                                                                                                                                                                                       - by cultivating Escherichia coli ATCC 39613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High yield streptokinase A prodn. from infected bacteria - contg. recombinant phage including gene from Streptococcus, useful as thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptokinase A from Streptococcus pyogenes SF130/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB
llarity 100.0%; Pred. No. 82;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR06378 standard; protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEAK ) AKAD WISSENSCHAFTEN DDR
                                                                                                                                                                                                                             Streptokinase prodn. – by culti
contg. recombinant plasmid pMF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 7pp; German
                                                                                  (PHIP ) PHILLIPS PETROLEUM CO. (UYOK-) UNIV OF OKLAHOMA.
                                                                                                                                                                                                                                                                                Example; Fig 2; 28pp; English
          84US-0585417.
83DD-025553.
83DD-0255235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88DD-0321532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88DD-0321532.
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(first entry)
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                                                                                                                                     Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walter F, Siegel M,
                                                                                                                                                                        WPI; 1985-135032/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-247328/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ05604
                                                                                                                                                                                          N-PSDB; AANS0493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY
              02-MAR-1984;
10-OCT-1983;
10-OCT-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1988;
                                                                                                                                       Ferretti JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
20-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR06378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel thrombolytic agent comprising streptokinase where at least one nonessential portion has been modified. The invention also describes a method of forming a thrombolytic agent comprising determining a nonessential portion of streptokinase and modifying the nonessential portion to render the resulting protein less antigenic. The modified streptokinase is used to treat blood clot disorders, such as heart attacks. The modified streptokinase has less antigenicity than streptokinase but is still able to complex plasminogen and lead to plasminogen activation. Modified streptokinase with the nonessential portions removed or trundated simplify the molecule. Such smaller proteins are cheaper and easier to produce. This sequence represents a fragment of a Streptococcus sp. streptokinase protein which is used in the description of the method of the invention.
                                                                 Thrombolytic agent; streptokinase; antigenic; blood clot; heart attack;
                                                                                                                                                                                                                                                                                                                                                                                                         New thrombolytic agents derived from modified humanized streptokinase, useful for treating blood clot disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoded by skc streptokinase gene on the 2.5kb PstI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ົວ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus equisimilis strain H46A (serological group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                Streptococcus sp. streptokinase protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzyme; thrombolytic agent; blood clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 48-49; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP50620 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                  (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                               99WO-US10086
                                                                                                                                                                                                                                                                 98US-0084392
                                                                                                                                                                                                                                                                                                                                     Lin X, Tang JJN
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            produced pMF1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SVDVEY 6
                                                                                                                                                         WO9957251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-1984;
                                                                                                                          Ното варіепв
                                                                                                                                                                                                                               06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1991
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9
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                                                                                                                                                                                                                                                                                                                                       Zhang XC,
                                                                                       treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Gaps

Gaps

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Indels

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Length 440;

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100.0%; Score 30; DB
llarity 100.0%; Pred. No. 82;
Conservative 0; Mismatches
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89GB-0027722
                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-208151/28
                                                                 183 SVDVEY 188
 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 AA
                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ12156
                                              SVDVEY
                                                                                                                                                                                                   Streptokinase.
                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Formation is
                                                                                                                                                                 25-MAR-2003
17-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                             WO9109125-A
                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dawson KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                              AAR12889;
                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                              Protein
                                                                                                   RESULT 48
                                                                                                             AAR12889
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid pWM1 (contg. the streptokinase G gene ) is ligated with pUC19 and the resultant product used to transform bacteria. Infected cells are cultured in lig. medium contg. assimilable C and N sources, and streptokinase G is isolated from the cell lysate.

The infected cells provide the protein in high yields, i.e. 600 U/ml which is 1.5-2 times that for the donor strain.

The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thrombolytic agent. See also DD-276694 (AAQOS604).

(Updated on 25-MAR-2003 to correct PA field.)
              Lambda 147.1 is ligated with genomic DNA from S. pyogenes SF130/13 and the resultant product used to transform bacteria. Infected cells are cultured in liq. medium contg. assimilable C and N sources, and streptokinase A is isolated from the cell lysate. The infected cells provide the protein in high yields, i.e. 1000 U/ml compared to 80 U/m; for the donor strain. The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thronbolytic agent. See also DD-276693 (AAQ05603).
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High yield streptokinase G prodn. from recombinant cells -
transformed with plasmid contg. gene from Streptococcus, useful
                                                                                                                                                                               0
                                                                                                                                                   100.0%; Score 30; DB 11; Length 440; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                       Streptokinase G protein from Streptococcus pyogenes G19908.
                                                                                                                                                                                                                                                                                                                                                                             Streptokinase G; thrombolytic agent; plasminogen; plasmin;
                                                                                                                                                                               Indels
                                                                                                                                                                                .
0
                                                                                                             (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                AAR06377 standard; protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEAK ) AKAD WISSENSCHAFTEN DDR
                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walter F, Siegel M, Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88DD-0321531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88DD-0321531.
                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-247327/33.
                                                                                                                                                                                                                                                                                                                                                                                          recombinant plasmid
                                                                                                                                                                                                                         SVDVEY 188
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                       440 AA;
                                                                                                                                                                                                    1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1988;
                                                                                                                                                                                                                                                                                                                         25-MAR-2003
20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                     DD276693-A
                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                      AAR06377;
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                            RESULT 47
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         XSSSSSSSSSSXX
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The sequence was deduced from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C ) ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H66A (Malke, H., Roe, B., and Perretti, J.J., Gene 34 357-362 [1985]). See Swiss-Prot K02986 and P00779 and Geneseq N70106. The gene can be used to construct expression eccord in which the streptokinase gene is linked to a second gene encoding e.g. another streptokinase protein, hirudin, or a streptokinase-like protein, via a linking sequence encoding a cleavage site for e.g. factor Xa or thrombin. The enzymes which cleave the fusion protein are present at the site of the target thrombus so the active agents are released specifically at the place where clot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Length 440;
                                                                                                                                                                                                                                                                                                                   Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n is occurring.
R12887, R12888, R12891-R12894, R12885 and R12522
on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                           equisimilis ATCC 9542 or ATCC 100009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27..440
/label= mature streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...26
'label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 80; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
AAR12889 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRBI-) BRITISH BIO-TECHNOLOGY LTD
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100.0%;
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Best Local Similarity
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||||||| 183 SVDVEY 188

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AAR12885 standard; Protein; 483 AA.
                                        RESULT 50
AAR12885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. [1], mucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactica and S. pyrogenes. Nucleic acids encoding (1) are used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be cused as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                                                                                    Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus, Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
 Gaps
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 Indels
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 Mismatches
                                                                                                                                                                Streptococcus polypeptide SEQ ID NO 8298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3946; 4525pp; English.
                                                                                                   ABP29561 standard; Protein; 440 AA
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                                                                                                                                                                                                                                                                                                                         27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                    29-OCT-2001; 2001WO-GB04789.
                                                                                                                                              02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
  6; Conservative
                                                                                                                                                                                                                                     Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-352536/38.
N-PSDB; ABN70192.
                                            183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 AA
                        1 SVDVEY 6
                                                                                                                                                                                                                                                         WO200234771-A2.
                                                                                                                                                                                                                                                                                02-MAY-2002.
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Tettelin H;
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                                                                                                                         ABP29561;
   Matches
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The protein is a recombinant product of a gene fusion construct.

The sequence of the synthetic hirudin HV-1 genes was designed

The sequence of the synthetic hirudin HV-1 genes was designed

Enters 165 180 (1984).

Letters 165 180 (1984).

The sequence (both as sequence of streptokinase was obtd.

From PCR samplified chromosomal DNA from S. equisimilis ATCC 10009

C or ATCC 9642.

The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H. Roe, I ished DNA sequence of S. equisimilis strain H46A (Malke, H. Roe, I ished DNA sequence of S. equisimilis strain H46A (Malke, H. Roe, I ished DNA sequence were used to construct an expression vector in which the hirdin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring.

See also AAR12887-R12889, AAR12891-R12894 and AAR12522.
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                                                                                                                                                                                              Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     66..69
/label= linker
/note= "factor Xa cleavage site"
                                                                                                                                         Factor Xa-cleavable hirudin-IEGR-streptokinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70..483
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..65
/label= hirudin HV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 96; 115pp; English.
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89GB-0027722.
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                                                        (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ12162
                                                        25-MAR-2003
17-SEP-1991
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07-DEC-1989;
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                                                                                                                                                                                                                                                                                                     Synthetic
AAR12885;
                                                                                                                                                                                                                                                                                                                                                                    Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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Best Local Similarity 100. Matches 6; Conservative

Query Match

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Gaps

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100.0%; Score 30; DB 23; Length 440; 100.0%; Pred. No. 82; ive 0; Mismatches 0; Indels (

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1 SVDVEY

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AAR1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The protein is a recombinant product of a gene fusion construct.

The sequence of the synthetic hirudin HV-1 genes was designed
assed on the published amino acid sequence (bodd J., et al FBBS)

Letters 165 180 (1984). The sequence of streptchinase was obtd.

Cor APCC 9642. The primers used for the PCR were based on the published bunks are used for the PCR were based on the published bunks are used to construct an expression vector in which the sequence encoding a cleavage site for factor Xa. The factor Xa is sequence encoding a cleavage site for factor Xa.

Cor APCC 10009

Cor APCC 9642. The primers used for the bunks of the two is sequence used to construct an expression vector in which the streptchinase gene is linked to the hirudin gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are creased specifically at the place where clot formation is occurring. See also AAR12889. ARA12891-R12894 and AAR12885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion protein cleavage by blood clotting enzyme - for prodn. of
fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 100.0%; Score 30; DB 12; Length 483; Similarity 100.0%; Pred. No. 91; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis.
                                                                                                                                                                                                                                                                      /label= linker
/note= "factor Xa cleavage site"
                                                                                                                                                  Factor Xa-cleavable streptokinase-IEGR-hirudin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Czapleswski LG;
                                                                                                                                                                                                                                         1..414
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 96; 115pp; English
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           (BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                        AAR12522 standard; Protein; 483 AA
                                                                                                                                                                                                                                                                                            419..483
/label= hirudin
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89GB-0027722.
                                                                                                                                                                                                                                                                                                                                                                       90WO-GB01911
                                                                                                                   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserval
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                    226 SVDVEY 231
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SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                            37-DEC-1990;
                                                                                                                   25-MAR-2003
17-SEP-1991
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                                                                                                                                                                                                         Synthetic
                                                                                                AAR12522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The streptokinase sequence was obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642 (the primers used for the PCR were based on the published DNA sequence, G. equisimilis strain H46A (Malke, H., Roe, B., and Perretti, J.J., Gene 34 357-362 [1985]). The gene was fused to DNA encoding the yeast alpha factor pre-pro-secretion sequence in an expression vector, pSMD1/152, for prodn. of recombinant streptokinase in S. cerevisiae strain BJ2168. See also ARR12887-R12885, AARR12892-R12984, AARR12885 and AARR12522. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pusion protein cleavage by blood clotting enzyme - for prodn. of
fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                              1..85
/label= pre-pro alpha factor secretion sequence
/note= "S. cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                             Streptokinase fused to yeast alpha factor secretion sequence.
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                                                                                                                                                                                                                                Pusion protein; blood clotting; coagulation; fibrinolysis;
antithrombotic; thrombolysis; streptokinase.
                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis ATCC 9542 or ATCC 100009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86..499
/label= mature streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Czapleswski LG;
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                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
AAR12891 standard; Protein; 499 AA.
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89GB-0027722.
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                                                                                                        (updated)
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                                                                                                        25-MAR-2003
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                                                        AAR12891;
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Best Local S
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Peptide
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Matches
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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition comprising an isolated modified streptokinase, the composition comprising an isolated modified streptokinase, the composition comprising an isolated modified streptokinase, the modification being removal of animo acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a duninistering to the subject a fibrin-dependent streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis graft thrombosis and atterial thrombosis. Streptokinase can also be used in non-human mammals. Streptokinase can also be used in non-human mammals. Streptokinase completed streptokinase has at least to fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin than in the discreptivition that inactivates a substrate site for proteclytic cleavage. This reduces the inactivates a substrate site for proteclytic cleavage. This reduces the sequence represents recombinant streptokinase at least two-fold The present sequence represents recombinant streptokinase, designated risked 414.
myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis, arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein, blood clotting; coagulation, fibrinolysis; antithrombotic, thrombolysis; streptokinase; thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus equisimilis ATCC 9542 or ATCC 100009,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 30; DB 20;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Met-core streptokinase-core streptokinase.
                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 55-58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR12894 standard; Protein; 747 AA.
                                                                                                                                                                                                                                                                                                                                         N-terminally deleted streptokinase
                                                                                                                                                            98WO-US26694
                                                                                                                                                                                           97US-0069497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Match
Best Local Similarity 100....
Best Accessive
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(first entry)
                                                Streptococcus equisimilis
                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                        WPI; 1999-395183/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||
SVDVEY 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVDVEY 6
                                                                                                                                                                                                                                                                                                          N-PSDB; AAX83589
                                                                                                                                                              .5-DEC-1998;
                                                                                                 409931247-A1
                                                                                                                                                                                            15-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
17-SEP-1991
                                                                                                                                24-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR12894;
                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479
                                                                                                                                                                                                                                                            Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR12894
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Imparting injectable fibrinolytic agent - with affinity for intravascular thrombus, by linking agent to fibrin binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The conjugate comprises an FB-FB dimer linked to streptokinase The FB fragment has selective affinity for fibrinogen, and minimal immunogenicity, imparting thrombustargetting capability. See also AAR11821 and AAR11828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 100.0%; Score 30; DB 12; Length 531; Local Similarity 100.0%; Pred. No. 1e+02; les 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                               Fibrin-binding protein; fibrinolysis; intravascular thrombi; fibrinogen; streptokinase; fusion protein.
                                                                                                                                                                                                                                                                                         62..119
/label= PB monomer
120..531
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant streptokinase rSK60-414
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24798 standard; Protein; 736 AA.
                                                                                                                                                                                                                                                               2..61
/label= FB monomer
                                     AAR11829 standard; Protein; 531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 5, 18pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87US-0099242
89US-0437769
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                                                                                                      08-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CREA-) CREATIVE BIOMOLEC.
                                                                                                                                   FB-FB-SK fusion conjugate
                                                                                                                                                                                                                  Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-140198/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 SVDVEY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ11651
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                           US5011686-A
                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pang RHL;
                                                                       AAR11829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                             Peptide
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Gaps

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Key Protein

Protein

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induces fibrin-dependent plasminogen activation in a pharmaceutical composition comprising an isolated modified streptokinase, the composition comprising an isolated modified streptokinase, the modification being removal of anion acid residues in the amino terminus.

(2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; anuclaic acid (1) encoding a modified bacterial streptokinase protein; capression vector comprising (1); and (4) a host cell transformed with expression vector comprising (1); and (4) a host cell transformed with a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, creebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least to effect protectolytic cleavage. The modified creeptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. The present creptesents a streptokinase at least two-fold. The present sequence represents a streptokinase at least two-fold. The present sequence represents a streptokinase at least two-fold. The present sequence represents a streptokinase and maltose binding protein fusion protein from an example of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated bacterial protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen-binding fragment; streptokinase; degradation;
thrombolytic agent; blood clot; bolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 20;
1larity 100.0%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen-binding domain from streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW21723 standard; protein; 800 AA.
                                                                                                                                                                                                                                                                                                                                                                                N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 48-51; 73pp; English
                                                                                                                                 98WO-US26694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis.
                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                  WPI; 1999-395183/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 SVDVEY 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  795 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX80497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9641883-A1.
                                                                                                                                                                           15-DEC-1997;
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                                                                                                                                    15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                            WO9931247-A1
                                                                                        24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW21723;
  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW21723
음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence was deduced from DNA obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642. The gene was tuncated by 15 codons at the 3' terminal and one copy engineered to add a Met codon prior to codon 16 of the CDS. The two truncated genes were used to construct an expression vector in which they were linked via a sequence encoding a cleavage site for thrombin which, when cleaved, releases the individual proteins which have antithrombotic activity. The thrombin is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12893, AAR12885 and AAR12522. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein cleavage by blood clotting enzyme - for prodn. of
fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 30; DB 12; Length 747; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptokinase and maltose binding protein fusion protein.
                                                                                                                      370.379
/label= thrombin cleavage site
                                                2.369
/label= core streptokinase
/note= "AAs 16-383"
                                                                                                                                                           380.747
/label= core streptokinase
/note= "AAs 16-383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 93; 115pp; English
                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY24797 standard; Protein; 795 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRBI-) BRITISH BIO-TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                90WO-GB01911
                                                                                                                                                                                                                                                                                                                                                                                         90WO-GB01911
89GB-0027722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-208151/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ12161
                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                  07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                              37-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1989;
                                                                                                                                                                                                                                                            WO9109125-A.
                                                                                                                                                                                                                                                                                                        27-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dawson KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Gaps

Matches

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Gaps

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The streptokinase sequence was obtd, from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The gene was used to construct an expression vector in which two streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and prophylaxis.
                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; major outer membrane protein A;
of streptokinase. This fragment was used in the design of a modified streptokinase has an in vitro degradation rate at le 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus rather than by continuous infusion.
                                                                                                                                         Length 813;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus equisimilis ATCC 9542 or ATCC 100009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436..445
/label= linking peptide
/note= "cleavage site for thrombin"
                                                                                                                                           100.0%; Score 30; DB 18;
100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÿ
                                                                                                                                                                                                                                                                                                                                                                                                           OmpAL streptokinase-streptokinase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..21
/label= OmpAL signal a
/note= "from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22..435
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Czapleswski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 90; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                   AAR12893 standard; Protein; 859 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90WO-GB01911
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                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-208151/28
                                                                                                                                                                                                                               SVDVEY 161
                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                  813 AA;
                                                                                                                                                                                                    1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ12160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1990;
07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombin; as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                  AAR12893;
                                                                                                                                                                                                                                 156
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                            RESULT 59
AAR12893
                                                                                                                                                                        Matches
                                                                                                                                                                                                                               요
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment
                                                                                                                                                                                                                                           This sequence represents the plasminogen-binding fragment of streptokinase which lacks the N-terminal 14 amino acids. This modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                           Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild type plasminogen-binding fragement of Streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 18;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 12-13; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW21728 standard; protein; 813 AA.
                                                                                                                                                                                                                   Claim 2; Page 35-37; 65pp; English
                                                                                                                                                                                                                                                                                                                                                   rather than by continuous infusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US09640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0488940
                    96WO-US09640
                                               95US-0488940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                           (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE
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                                                                                                                                   WPI; 1997-065469/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                800 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1995;
                    07-JUN-1996;
                                                09-JUN-1995;
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                                                                                                                                                                                            equipment
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW21728
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                         Reed GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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This sequence represents the wild type plasminogen-binding fragment

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                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
genes are linked via a sequence encoding a cleavage site for thrombin which, when cleaved, releases the individual proteins which have anti-thrombotic activity. The thrombin is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12894, AAR12885 and AAR12522. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase/maltose binding protein fusion protein, rSKdeltal4
                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasminogen-binding fragment; streptokinase; degradation; MBP;
thrombolytic agent; blood clot; bolus; maltose-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Has N-terminal 14 amino acids deleted"
                                                                                                                                                         100.0%; Score 30; DB 12; Length 859; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.381
/label= Maltose binding protein
/note= acts as blocking group"
382.1181
/label= Modified_Streptokinase
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                    AAW21727 standard; protein; 1181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 12; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus equisimilis.
                                                                                                                                              Query Match
Best Local Similarity 1000.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-065469/06.
                                                                                                                                                                                                                                                      178 ŚVDVEY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1181 AA;
                                                                                                                                 859 AA;
                                                                                                                                                                                                                         1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1996;
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                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                       RESULT 60
AAW21727
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
                                                                                                                                                                                                                                        Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein.
                        ö
 Length 1181;
                         Indels
100.0%; Score 30; DB 18;
100.0%; Pred. No. 2.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              ..381
|abel= Maltose_binding_protein
|note= "acts as_blocking_group"
                                                                                                                                                                                                                                                                                                                                                                                label= Modified_streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 41-44; 65pp; English.
                                                                                                                                       AAW21724 standard; protein; 1194 AA.
                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                 Modified streptokinase, rSK5mut
                                                                                                                                                                                                                                                                                                                                                                                                         label= R10A
                                                                                                                                                                                                                                                                                                                                                                                                                                label= R36A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= R45A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= R51A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0488940
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                              Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                   .1194
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 39
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                                                   1 SVDVEY
                                                                            524 SVDVEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39-JUN-1995;
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9
                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equipment
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                                                                                                                                                                                                                                                                                                                                Protein
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                           Matches
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Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
equipment
                                                                                                   Plasminogen-binding fragment, streptokinase, degradation, MBP, thrombolytic agent, blood clot, bolus, maltose-binding protein.
          AAW21725 standard; protein; 1194 AA.
                                                                             Modified streptokinase, rSK6mut.
                                                        (first entry)
                                                                                                                                    Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-065469/06.
                                                                                                                                                                                                                                                                                                                                Misc-difference 440
                                                                                                                                                                                                                                                                                  Misc-difference 426
                                                                                                                                                                                                                                                                                                          Misc-difference 432
                                                                                                                                                                                                                                                             Misc-difference 417
                                                                                                                                                                                                                                        Misc-difference 39:
                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1996;
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                                                      01-OCT-1997
                                                                                                                                              Synthetic.
                                 AAW21725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed GL;
                                                                                                                                                                                 Protein
                                                                                                                                                                                                                   Protein
AAW21725
ID AAW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a fusion protein between maltose-binding protein and the plasminogen-binding fragment of streptokinase. This fusion protein was used in the design of modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood colots in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
equipment
                                ö
                                                                                                                                                                                                                           Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein.
         Score 30; DB 18; Length 1194;
Pred. No. 2.5e+02;
; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 100.0%; Score 30; DB 18; Length 1194; Local Similarity 100.0%; Pred. No. 2.5e+02; nes 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                     Streptokinase/maltose binding protein fusion protein, rSK
                                                                                                                                                                                                                                                                                           1.381
/label= Maltose binding protein
/note= "acts as blocking group"
382.1194
/label= Streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 11-12; 65pp; English.
                                                                                                                                   AAW21726 standard; protein; 1194 AA.
                                                                                                                                                                                                                                                                                 Location/Qualifiers
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0
         Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0;
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                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                            Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-065469/06.
                                                                            537 SVDVEY 542
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                                                      1 SVDVEY
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                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                             RESULT 62
                                                                                                                         AAW21726
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/label= K385A /note= "Given in the specification as K386A"

96WO-US09640 95US-0488940

label= R59A

/label= Maltose binding protein /note= "acts as blocking group" 382.1194 /label= Modified_streptokinase

label= R36A label= R45A label= R51A

/label= R10A

Location/Qualifiers

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                                                    This sequence represents a fusion protein between maltose-binding protein and a modified form of the plasminogen-binding fragment of streptokinase containing 6 point mutations. This modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agence for dissolving blood closs in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion.
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                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 18; Length 1194; 100.0%; Pred. No. 2.5e+02; Live 0; Mismatches 0; Indels 0.
Claim 16; Page 44-48; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                537 SVDVEY 542
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                    Sequence 1194 AA;
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Gaps

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SVDVEY 542

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RESULT

1 SVDVEY 6

Best Loc Matches

Search completed: January 20, 2004, 14:58:47 Job time : 42 secs

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2004, 13:54:52; Search time 42 Seconds (without alignments) 22.675 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gcgdata/geneseq-geneseqp-embl/AA2001.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | Streptokinase deri | Streptokinase deri | | | | | | | |
|------------|-------------|--------------------|--------------------|----------|----------|----------|----------|----------|----------|----------|
| SUMMARIES | a . | AAY25009 | ABB80001 | ABB80005 | AAY25013 | AAY25014 | ABB80006 | ABG76052 | AAY25015 | ABB80007 |
| | 8 | 20 | 23 | 23 | 20 | 50 | 23 | 24 | 20 | 23 |
| * Query | Length | φ | 9 | 16 | 18 | 20 | 20 | 20 | 21 | 21 |
| * Query | Match | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| | Score | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 |
| Result | No. | 1 | 7 | m | 4 | υ | œ | 7 | œ | σ |
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| itope | uodse | 35.5 | espon | , ~ | strep | t str | Streptokinase (1-3 | d 5 | - T) = | ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;; | 귷 | a) | ğ., | a) (| p e | Representative str | Streptokinase enco | S.equisimilis stre | Streptokinase. St | Streptococcus equi | Streptococcus equi | Streptococcus equi | Streptokinase (SK) | De-1mmunised strep | Wild type streptok | Altered streptokin | Mutant streptokina | Streptococcus plas | Streptococcus sp. | Sequence encoded b | (D | | od e | | eaves e fus | ion | | eptok and | | semin | kina (| Streptoxinase/mait | э/па] | þ | alano | alano | Streptokinase deri | 4 6 | yay | چ. | 5 | <u> </u> | mbra | | |
|-----------|-----------|-----------|-----------|------------|-----------|-----------|--------------------|-----------|-----------|----------------------------------------|-----------|------------|-----------|-----------|-------------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-----------|-----------|-----------|-----------|----------------|-----------|-----------|--------------|-----------|-----------|-----------|--------------------|-----------|-----------|-----------|-----------|--------------------|---------|---------|-----------|-----------|----------|-----------|---------|--|
| 0 AAY0155 | 0 AAY0155 | 0 AAY2479 | S AAYO155 | S ARRELD | 0 AAY2479 | 2 AAR1289 | 2 AAR10195 | 2 AAR1019 | 2 AAK1020 | 2 AAR1019 | 1 AAY8400 | 2 AAR1019 | 1 AAY8400 | 0 AAY2502 | 1 AAY8400 3 ABBBA001 | 4 ABG7419 | 2 AAR1019 | 3 AAR2020 | 5 AAR6312 | 0 AAY2479 | 0 AAW9466 | 0 AAW9466 | 0 AAW8614 | 0 AAW8614 | 1 AAB0129 | 1 AAB0129 | 2 AAB7494 | 1 AAY9959 | 1 AAY5087 | AAFSU620 | 1 AAR0637 | 2 AAR1288 | 3 ABP2956 | Z AAKIZBB | 2 AAR1289 | 2 AAR1182 | 0 AAY2479 | 2 AAR1289 | B AAW2172 | 8 AAW2172 | 2 AAR1289 | B AAWZI/Z | 3 AAW2172 | 3 AAW2172 | 2 ABB6630 | 2 ABB5881 | AAYZSUL | ABG7419 | AAY5196 | L AAY5197 | 1 ABP6041 | AAU6479 | 3 AAW0674 | ABR3909 | |
| 71 | 46 | 200 | n r | ν 4 • α | 9 9 | 69 | 371 1 | 2 5 | 4 5 | 4 4 | 84 | 91 | 10: | η r | ٦ ۲ | n m | 14 | 14 | 14 | 4, 4 | 14. | 14 | 4. | 4, 4 | 1 4 | 4. | 14 | 51 | un c | 0 4 0 4 0 6 | 40 | 40 1 | 40 2 | 26 | 9 6 | 31 1 | 36 2 | 747 | 000 | 13 | 859 1 | 7 7 7 8 9 | 194 1 | 194 1 | 520 2 | 90 | N C | ١, | | 7 | 17 2 | 7 0 | 55. | 91 2 | |
| 00 | 00 | 90 | 96 | 9 6 | 88 | 8 | 100.0 | 96 | 9 8 | 88 | 8 | 00 | 9 8 | 9 6 | 9 6 | 88 | 00 | 00 | 8 | 9 8 | 80 | 80 | 99 | 96 | 96 | 90 | 00 | 99 | 9 8 | 9 6 | 88 | 80 | 90 | 9 6 | | 00 | 99 | 9 6 | | 00 | 9 6 | 3 8 | | 00 | ú. | | | | : .: | ·. | ٠. | | : - | | |
| 30 | 30 | 9 6 | 9 6 | 9 6 | 0 0 | 30 | 30 | 0 0 |) r | 0 0 | 30 | 30 | 30 | 9 6 | 9 6 | 200 | 30 | 30 | 30 | 9 6 | 90 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 0 6 | 30 | 30 | 30 | O C | 00 | 30 | 30 | 0 0 | 0 O | 30 | 90 | 9 6 | 0 0 | 30 | 29 | 53 | 77 | | 27 | 27 | 27 | 120 | 27 | 27 | |
| 10 | 11 | 12 | E . | 4 r | 110 | 17 | 18 | 6 C | 2 6 | 22 | 23 | 4. | 5.2 | 9 5 | 7 7 6 | 1 N 0 | 30 | 31 | 35 | | י נח ה ה | 36 | 37 | B 0 | 4 4 | 41 | 42 | 43 | ጭ ና ተ ከ | 4. 4 U A | 47 | 48 | 4, i | ر د د | 25 | 53 | 5.4 | 55 57 | 5.5 | 28 | 0.0 | 2 4 | 9 6 | 63 | 64 | 92 | 9 4 | o co | 69 | 70 | 71 | 73 | 74 | 75 | |

ALIGNMENTS

RESULT 1 AAY25009

Complex the series of the second states of the seco Streptokinase derived peptide 1 for amelioration of cell death. AAY25009 standard; peptide; 6 AA. 96US-0759599. 95US-0008233 96US-0759599 (first entry) Krystal G, Rabkin SW; WPI; 1999-394231/33 (RABK/) RABKIN S W. 06-DEC-1995; 05-DEC-1996; 05-DEC-1996; 23-AUG-1999 US5917013-A. 29-JUN-1999 AAY25009;

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation Claim 2; Column 12; 15pp; English.

AAY25009-Y25019 are novel peptides derived from streptokinase that

C ameliorate cell death. The products of the invention and their encoding

C nucleic acids may be useful for treating diseases and conditions related

to aging, cellular differentiation, physical insult (e.g. physical

CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

and any other organ), viral disorders (e.g. hepatitis, retroviral

infections, viral encephalitis, and ADDS/HIV), neurodegenerative

CC disorders (e.g. parkinson's disease, Alzheimer's disease, Huntington's

disorders (e.g. parkinson's disease, Alzheimer's disease, Huntington's

CC disease, cerebellar degenerations, and familial amyotrophic lateral

sclerosis (FALS), cardiovascular disease (e.g. atherosclerosis,

CC myocardial infarction, heart fallure, cardiomyopathy, myocardial

reperfusion injury, and hypertensive heart disease, insulin-dependent,

creperfusion injury, and hypertensive heart disease, insulin-dependent,

diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema

condosum, Sjogene's syndrome, temporal arthritis, myasthenia gravie,

wegener's granulomatosis, glomerulomephritis, anti-phospholipid syndrome,

cand autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,

csarcomas, myedomas, cardiomomas, melanoma, cancers of the

breast, brain, colon, cervix, and prostate, Hodgkin's disease and

chor-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint

disorders and inflammatory induced cell damage to the eye, brain and

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

WPI; 2002-266542/31.

Claim 3; Column 5; 18pp; English

ô Whenevoprotective, antiparkinsonan, articonvulsant; cytostatic;

Antinflammatory; antiarkinsonan; anticonvulsant; cytostatic;

Antinflammatory; antiarkhritic; antirheumatic; cardiant;

Whenevoprotective; antidateriz; antiamemic; virucide; ophthalmological;

Whenevological; antidaterial; antiparasitic; virucide; ophthalmological;

Whenevological; antidaterial; antiparasitic; heurodegenerative disease;

Whenevological; antidaterial; inflammatory disease;

Wherebellar degeneration; arthritis; inflammatory joint disorders;

Wherebellar reperfusion injury; immune disease; autoimmune disease;

Whocardial reperfusion injury; immune disease; autoimmune disease;

Why acquired immunodeficiency syndrome; AlDS; rheumatoid arthritis;

Why systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;

Why systemic lupus diseases; viral diseases; macular degeneration;

Why caractist crohn's diseases; viral diseases; macular degeneration;

Why correction crohn's diseases; uncerative colitis; pancreatitis; other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia or infarction, and stroke), toxic insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxious substances), macular degeneration, cataract formation, pancreatitis, Crohn's disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT, Gaps .. 0 100.0%; Score 30; DB 20; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels Streptokinase; cell death; apoptosis; necrosis; nootropic; (MOLE-) MOLECULAR THERAPEUTICS INC. ABB80001 standard; peptide; 6 AA. Streptokinase derived peptide#1. 99US-0294457. 95US-008233P. 96US-0759599. (first entry) Conservative Krystal G, Rabkin SW; prion disease; aging and anthracyclines. Best Local Similarity Matches 6; Conserv 1 SVDVEY 6 6 AA; 1 SVDVEY US6348567-B1 26-JUL-2002 19-APR-1999; 06-DEC-1995; 05-DEC-1996; 19-FEB-2002. Synthetic. Sequence ABB80001; Query Match ABB80001 ઠે

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as a noctropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiparkristic, antirheumatic, cardiant, antinflammatory, antiparkristic, immunosuppressive, anti-HIV decreated particulabetic, antianemic, virucide, ophthalmological, antiulcer, antibacterial and antiparasitic. Peptides of the invention ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. perkinson's, Alzheimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. archritis, inflammatory joint calsorders), cardiovascular diseases (e.g. pheat fallure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases (e.g. autoimmune diseases (e.g. autoimmune diseases), and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases (e.g. autoimune diseases en diseases (e.g. autoimune diseases en diseases of any organ. Other disorders include macular degenerative diseases of any organ. Other disorders include macular degenerative diseases of any organ. Other disorders include macular degenerative diseases and diseases including bacteria, parasite, prion-based diseases, and accelerated aging. The current sequence represents a streptokinase disease, including contents and with an ability to ameliorate cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death in cardiac myocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AA;
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Length 6; 0; Indels 100.0%; Score 30; DB 23; 100.0%; Pred. No. 9.3e+05; Mismatches . 0 Local Similarity 100. Les 6; Conservative 9 1 SVDVEY 6 1 SVDVEY Query Match 8 g

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Gaps ; 0

> ABB80005 standard; peptide; 16 AA Streptokinase derived peptide#5. (first entry) 26-JUL-2002

Streptokinase, cell death, apoptosis, necrosis, nectropic;

meuroprotective, antiparkinsonian, anticonvulsant, cytostatic;
mutinfiammatory, antiarthritic; antirhematic; cardiant,
antiatherosclerotic; vasotropic; immunosuppressive, anti-HIV;
dermatological; antidabetic; antimanaemic; virucide; ophthalmological;
antiulcer; antibacterial, antiparasitic; neurodegenerative disease;
A parkinson's disease; Alzheimer's disease; Huntington's disease;
merebellar degeneration; neoplastic disorder; cancer;
inflammatory disorder; arthritis; inflammatory joint disorders;
my cardiantory disorder; arthritis; inflammatory joint disorders;
my cardial reperfusion injury; immune disease;
acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;
systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;
myelodegenerative diseases; ulcerative colitis; pancreatitis; prion disease; aging

Synthetic

19-FEB-2002

99US-0294457 19-APR-1999;

95US-008233P. 96US-0759599. 06-DEC-1995; 05-DEC-1996;

(MOLE-) MOLECULAR THERAPEUTICS INC

Krystal G, Rabkin SW,

WPI; 2002-266542/31.

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

Claim 7; Column 5; 18pp; English.

peptides of the invention may be described as, mostropic, concurrent of may be described as, mostropic, antinflammatory, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiarthritic, antirheumatic, cardiant, contrained antiarthritic, antiaressive, anti-MIV dermatological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, peptides of the invention ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating concurrents inflammatory disorders (e.g. heart is, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer: inflammatory disorders (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune conservation injury), immune diseases (e.g. autoimmune systemic lupus erythematosus, diabetes mellitus, permicious anaemia), myolodegenerative diseases, viral diseases, and degenerative diseases of myorden contrain, and diseases, undertained in parafic myorders, and edgenerative diseases, viral diseases, and degenerative diseases, contrained in parafic manning manning manning manning manning and mine contrains and manning and mine contrains contrains parafacts, and degenerative diseases. The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, diseases including bacteria, parasite, prion-based diseases, and accelerated aging. The current sequence represents a streptokinase derived peptide of the invention with an ability to ameliorate cell death in cardiac myocytes.

16 AA; Sequence

Gaps . 0 100.0%; Score 30; DB 23; Length 16; 100.0%; Pred. No. 1.9; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 6; Conservative

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1 SVDVEY 1 SVDVEY

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RESULT 4

AAY25013 standard; peptide; 18 AA. AAY25013

AAY25013;

(first entry) 23-AUG-1999 Streptokinase derived peptide 5 for amelioration of cell death.

Wegenerical death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; whypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; wiral disorder; heart; lung; liver; skin; HIV; wiral disorder; heartisis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; cardiovascular disease; was familial amyorophic lateral solerosis; atheroselerosis; heart failure; infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; we pernicious amemaia; dermatomyositis; enythema nodosum; myasthenia gravis; Sjogren's syndrome; temporal arthritis; auti-phospholipid syndrome; meoplastic disorder; leukemia; sarcoma; myasloma; neuromma;

melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline.

Synthetic

US5917013-A.

29-JUN-1999

96US-0759599 05-DEC-1996;

95US-0008233. 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Krystal G, Rabkin SW;

WPI; 1999-394231/33.

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 6; Column 12; 15pp; English.

XX XX AV25009-Y25019 are novel peptides derived from streptokinase that commeliorate cell death. The products of the invention and their encoding nucleic acids may be useful for treating diseases and conditions related to aging, cellular differentiation, physical insult (e.g. physical conditions related to aging, cellular differentiation, physical insult (e.g. physical conditions related to aging, cellular differentiation, physical insult (e.g. physical conditions related to and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin and any other organ), viral encephalitis, and AIDS/HIV), neurodegenerative disease, cerebellar degenerations, and AIDS/HIV), neurodegenerative disease, cerebellar degenerations, and familial amyotrophic lateral corposis (FALS), cardiovascular disease (e.g. atherosclerosis, collections, and Mypertenaive heart disease), immune disease (e.g. myocardial infarction, heart failure, cardiomyopathy, myocardial creperfusion injury, and hypertenaive heart disease), immune disease (e.g. reperfusion injury, and hypertenaive heart disease), immune apolyarthritides), a neoplastic disorder (e.g. luckemia, diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema of autoximmune polyarthritides), a neoplastic disorder (e.g. luckemia, sarcionas, myelomas, carcinomas, melanoma, cancers of the breast, brain, colon, cervix, and prostate, hodgkin's disease and con-Hodgkin's lymphoma', inflammatory disorders (e.g. inflammatory joint corposates, brain, colon, cervix, and prostate, hodgkin's disease and corposate, brain, colon, cervix, and prostate, hodgkin's disease and corposate, brain, colon, cervix, and prostate, hodgkin's disease and corposate, brain and inflammatory induced cell damage to the eye, brain and corposate, brain and erroke), inclammatory dischemia and corposate, brain, and prostate, brain and erroke), inclammatory dischemia and corposate, brain, and erroke), and erperfusion injury, retinal ischemia or infarction, and stroke), conditis, accelerative or insult cori neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT,

Sequence

Gaps ö 100.0%; Score 30; DB 20; Length 18; 100.0%; Pred. No. 2.2; tive 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 6; Conserv

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SVDVEY SVDVEY

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XX Streptokinase, cell death, amelioration; treatment; disease, aging; AIDS, Cellular differentiation; physical insult; trauma; anoxia; hyperthermia; XX byposthermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease, Alzheimer's disease; XX familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; XX familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; XX reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; XX pertemic lugus erythematosus; insulin-dependent; diabetes mellitus; XX pertemic lugus erythematosus; insulin-dependent; diabetes mellitus; y systemic lugus erythematosus; leutoimmune polyarthritides; hegener's granulomatosis; glomerulomephritis; anti-phospholipid syndrome; whosphastic disorder; leukemia; saccoma; myeloma; cancer; becast; colon; cervix; prostate; Hodokin's disease; hon-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; whon-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; such and ancer the syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. Streptokinase derived peptide 6 for amelioration of cell death. AAY25014 standard; peptide; 20 AA. (first entry) 23-AUG-1999 Synthetic. AAY25014; AAY25014

JS5917013-A.

29-JUN-1999

96US-0759599. 05-DEC-1996; 95US-0008233. 96US-0759599. 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Rabkin SW; Krystal G,

WPI; 1999-394231/33.

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 7; Column 12; 15pp; English.

AAY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

nucleic acids may be useful for treating diseases and conditions related
to aging, cellular differentiation, physical insult (e.g. physical

trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,
and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin
and any other organ), viral disorders (e.g. hepatitis, retroviral
infections, viral encephalitis, and AIDS/HV), neurodegenerative
disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's
disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's
clerosis (FALS), cardiovascular disease (e.g. atherosclerosis,
myocardial infarction, heart failure, cardiomyopathy, myocardial
cheumatoid arthitis, systemic lupus erythematosus, immune disease (e.g.
cheptitusion injury, and hypertensive heart disease), immune disease (e.g.
cheumatoid arthitis, systemic lupus erythematosus, insulin-dependent,
diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema
nodosum, Sjogren's syndrome, temporal arthitis, myasthenia gravis,
Megener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,
and autchimmune polyarthritides), a neoplastic disorder (e.g. leukemia,
sarcomas, myelomas, neuromas, melanoma, cancers of the

Claim 8; Column 5; 18pp; English.

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breast, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, real ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia or infarction, and stroke), toxic risult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxicus substances), macular degeneration, cataract formation, pancreatitis, Crohn's disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT,
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                                                                                                                                                                                                                              100.0%; Score 30; DB 20; Length 20; 100.0%; Pred. No. 2.4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptokinase; cell death; apoptosis; necrosis; nootropic;
                                                                                                                                                                                                                                                                                                                                                                              ABB80006 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                             and anthracyclines.
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                                                                                                                                                                                                      20 AA;
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20-MAY-2003
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                                                                                                                                                                                                                                   ABG76052;
                                                                                        RESULT 7
                                                                                                                            ABG76052
untinflammatory; antiparkinsonan; ancious, motivations, and antianflammatory; antiarthritic; antirheumatic; cardiant; antiatherosclerotic; vasotropic; immunosuppressive; antiatherosclerotic; vasotropic; immunosuppressive; antiatherosclerotic; variationaemic; virucide; ophthalmological; wantiulcer; antiabacterial; antiparasitic; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; Huntington's disease; warkinson's disease; Huntington's disease; minflammatory disorder; cancer; carcious disease; minflammatory disorder; arthritis; inflammatory joint disorders; wardiovascular disease; heart failure; atherosclerosis; myocardial reperfusion injury; immune disease; autoimmune disease; acquired immunodeficiency syndrome; AlDS; rheumatorid arthritis; systemic lupus erythematosus; diabetes mellitus; pernicious anaemia; mayelodegenerative diseases; ulcerative colitis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLE-) MOLECULAR THERAPEUTICS INC.
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96US-0759599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prion disease; aging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiparkinsonian, anticonvulsant, cytostatic, antinatherosclerotic, vasotropic, immunosuppressive, anti-HIV, cantidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiacers apoptosis and antiparasitic. Peptides of the invention ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions comprising peptides of the invention are useful for treating comprising peptides of the invention neoplastic disorders including cancer, inflammatory disorders (e.g. heart failure, atherosclerosis disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune cy systemic lugue erythematosus, diabetes mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases of any organ. Other disorders include macular degeneration, cataracts, myelodecrative diseases, viral diseases, and degenerative diseases, uccelerated aging. The current sequence represents a streptokinase collerated aging. The current sequence represents a streptokinase collerative diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atherosolarosais; myocardial infarction; immune disease; carcinoma; rheumatoid arthritis; mopolastic disorder; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; arthritis; inflammatory induced cell damage; motor neuron disease; physical insult; severe shock; ischaemia; reperfusion injury; heatitis; cost dath associated procedure; spinal cord reperfusion injury; toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease; duillain-Bare syndrome; bypass surgery; myocardial ischaemia; disease; bacterial disease; prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging; oxidative stress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase fragment based, cell death ameliorating, 20mer peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 23; Length 20; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG76052 standard; peptide; 20 AA.
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99US-0294457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death in cardiac myocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
6, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVDVEY
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19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
XXX66666666666666666666666666666688
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The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliorating cell death, its derivative or analogue, comprising a sequence Val-Asp-Val, where the peptide is in a suitable paramaceutical carrier or diluent. The pharmaceutical composition composition is a sequence of comprising the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's disease and Alzheimer's disease, cardiovascular disease e.g. Parkinson's disease and Alzheimer's neoplastic disorders e.g. leuksemia and carrinoma; inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and severe shock; inflammatory disorder e.g. arthritis and inflammatory induced cell caperfusion injury; toxic insult e.g. myocardial ischaemia and spinal cord reperfusion injury e.g. myocardial ischaemia and spinal cord controlly spinal cord disease e.g. motor neuron disease and Guillain-Bare syndrome; procedures associated with cell death e.g. bypass surgery and chemotherapy; viral disease e.g. hepatitis and viral encephalitis; infectious diseases e.g. hepatitis and viral encephalitis; clohn's disease; allocatarive colitis; accelerated aging and oxidative stress in a warm-binare fegence as a gener persents sequence represents the amino acid sequence as a gener peptide capable of ameliorating cell death which is based on a contract.
                                                                                                                                                                                                                                                      Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 3; 19pp; English.
96US-0759599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptokinase fragment
                                                                                                                                           Krystal G, Rabkin SW
                                                                                                                                                                                                   WPI; 2003-246673/25
                                                     (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
05-DEC-1996;
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20 AA; Sequence

Gaps . 0 DB 24; Length 20; 0; Indels Score 30; DB 2 Pred. No. 2.4; Mismatches . 0 100.0%; 6; Conservative Query Match Best Local Similarity Matches

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SVDVEY 1 SVDVEY

à g RESULT 8 AAY2501

AAY25015 standard; peptide; 21 AA. AAY25015;

Streptokinase derived peptide 7 for amelioration of cell death.

(first entry)

23-AUG-1999

Streptokinase, cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; bypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer s disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infarction; heart disease; carebellar degeneration; cardiovascular disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; pernicious anaemia; dermatomyositis; enylema modosum; myasthenia gravis; Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides; Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;

neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; pancreatits, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; clozapine; AZT; anthracycline.

Synthetic.

USS917013-A

29-JUN-1999

96US-0759599. 05-DEC-1996;

06-DEC-1995;

95US-0008233 96US-0759599 05-DEC-1996;

(RABK/) RABKIN S W.

Rabkin SW: Krystal G,

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 8; Column 12; 15pp; English

AAY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

nucleic acids may be useful for treating diseases and conditions related

to aging, cellular differentiation, physical insult (e.g. physical

to aging, cellular differentiation, physical insult (e.g. physical

conditions and creams to the brain, spinal cord, kidney, heart, lungs, liver, skin

and treams to the brain, spinal cord, kidney, heart, lungs, liver, skin

cand any other organ), viral disorders (e.g. hepatitis, retroviral

infections, viral encephalitis, and AlbS/HIV), neurodegenerative

disease, cerebellar degenerations, and familial amyotrophic lateral

cc disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's

disease, cerebellar degenerations, and familial amyotrophic lateral

cc disorders (FALS)), cardiovascular disease (e.g. atherosclerosis

myocardial infarction, heart failure, cardiomyopathy, myocardial

repertusion injury, and hypertensive heart disease, insulin-dependent,

cdiabetes mellitus, lupus, pernicious aneemia dermatomyositis, enythema

codosum, Sjogrem's syndrome, temporal arthritis, mysethenia gravis,

repenters mellitus, lupus, pernicious aneemia dermatomyositis, enythema

cc diabetes mellitus, lupus, pernicious aneemia, engeres of the

codosum, Sjogrem's syndrome, temporal arthritis, mysethenia gravis,

resence, myslomas, carcinomas, neuromas, melanoma, cancers of the

cc arcomas, myslomas, inflammatory disorders (e.g. inflammatory disorders and inflammatory induced cell damage to the eye, brain and

cother organs, issummatory induced cell damage to the eye, brain and

cother organs, issummatory induced cell damage to the eye, brain and

cother organs, issummatory induced cell damage to the eye, brain and

cother organs, issummatory induced cell damage to the eye, brain and

cother organs, issummatory induced cell damage to the eye, brain and

corgans from chemicals, retained aging, spinal cord issummatory degeneration, catarac and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT, and anthracyclines.

21 AA; Sequence

Gaps .. 0 100.0%; Score 30; DB 20; Length 21; 100.0%; Pred. No. 2.6; o; Mismatches 0; Indels 6; Conservative Best Local Similarity Matches 6; Conserv Query Match

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1 SVDVEY 6

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1 SVDVEY

accelerated aging. The current sequence represents a streptokinase derived peptide of the invention with an ability to ameliorate cell death in cardiac myocytes.

21 AA;

Sequence

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22223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase, cell death, apoptosis, necrosis, nootropic, neuroprotective, antiparkinsonian; anticonvulsant; cytostatic; antiantiantlammatory; antiarknistic; anticheuvalsant; cardiant; crimation antiatherosclerotic; vasotropic; immunosuppressive, anti-HTV; dermatological; antidabetic; immunosuppressive, anti-HTV; contidation antidabetic; antianammic; virucide; ophthalmological; continucer; antibacterial; antiparasitic; neurodegenerative disease; continucer; antibacterial; antiparasitic; neurodegenerative disease; crebellar degeneration; neoplastic disorder; cancer; inflammatory disorder; arthritis; inflammatory joint disorders; cardiovascular disease; heart failure; atherosclerosis; myocardial reperfusion injury; immune disease; autoimmune disease; cardiovascular disease; heart failure; atherosclerosis; cardiovascular continucersus; diabetes mellitus; pernicious anaemia; myelodegenerative diseases; viral diseases; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cataract; Crohn's disease; ulcerative colitis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR THERAPEUTICS INC.
                                                                                                                                                                                                  ABB80007 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Column 5; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase derived peptide#7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0294457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krystal G, Rabkin SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prion disease; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-266542/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS6348567-B1
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05-DEC-1996;
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                                                                                                 RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                           Gaps
                                                                                                                                                                                                                                                       Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis,
                                                                                                                                                                                                                              Antigenic epitope of streptokinase, spanning amino acids 138-208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 20; Length 71; 100.0%; Pred. No. 10;
 DB 23; Length 21;
                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevent or treat glomerulonephritis and rheumatic fever
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            2.6;
                           0; Mismatches
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100.0%; Score 30; 100.0%; Pred. No. 3
                                                                                                                                                AAY01550 standard; peptide; 71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 5; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0055911.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parhami-Seren B, Reed GL;
                                                                                                                                                                                                    18-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis.
                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-190113/16.
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Best Local Similarity
            Local Similarity
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                                                     1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AA;
                                                                             1 SVDVEY
                                                                                                                                                                                                                                                                                   rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                    WO9908698-A1
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                                                                                                                                                                          AAY01550;
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 Query Match
                Best Loc
Matches
                                                                                                                    RESULT 10
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RESULT 11 AAY01558

24-JUN-1999

AAY01558 standard; peptide; 146 AA

(first entry

18-JUN-1999

AAY01558

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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of animo acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising comprising to the subject a fibrin-dependent streptokinase; (3) an ancleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1), and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for a bacterial fibrin-dependent plasminogen activator is useful for composition, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial brombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase cutivation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The compilied streptokinase has at least one amino acid substitution that in activates a substrate site for proteolytic cleavage. This reduces the inactivates a substrate site for proteolytic cleavage. This reduces the sequence represents recombinant streptokinase, designated rSK144-293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 30; DB 20; Length 150; 100.0%; Pred. No. 24; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       Claim 34; Page 67-68; 73pp; English.
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                                                                                                                                                                                                                                                                                                              N-terminally deleted streptokinase
                                                                                                         97US-0069497.
                                                                98WO-US26694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US17114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                           1999-395183/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVDVEY 6
                                                                                                                                                                                                                                                                N-PSDB; AAX80494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatic fever
                                                                15-DEC-1998;
                                                                                                         15-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9908698-A1
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                                                                                                                                                                                                Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a peptide corresponding to amino acids 148-293 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. P1 is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                  Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis, rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                           Peptide corresponding to amino acids 148-293 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 20; Length 146; 100.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Disclosure; Page 13; 44pp; English.

Parhami-Seren B, Reed GL;

WPI; 1999-190113/16.

(GEHO) GEN HOSPITAL CORP. (HARD) HARVARD COLLEGE.

98WO-US17114 97US-0055911

18-AUG-1998; 18-AUG-1997;

Streptococcus equisimilis

WO9908698-A1

25-FEB-1999

Recombinant streptokinase rSK144-293

Streptococcus equisimilis

Synthetic

WO9931247-A1

(first entry)

26-AUG-1999

AAY24796 standard; Protein; 150 AA.

Query Match
Best Local Similarity 100.
Matches 6; Conservative

146 AA;

SVDVEY 15

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RESULT 12 AAY24796

1 SVDVEY 6

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Gaps

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Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and Arg 45 to Gly 68 also being deleted. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195 and AAR10197-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic gene encoding streptokinase - scale, high purity prodn.
of streptokinase used as a thrombolytic agent
                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 12; Length 348; llarity 100.0%; Pred. No. 63; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                 streptokinase; thrombolytic agent; myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ono K, Sakata Y,
                                                                                                                                                                                                                            AAR10196 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24795 standard; Protein; 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 59; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90JP-0096830.
89JP-0179432.
89JP-0307957.
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogino K,
                                                                                                                                                183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-016179/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
                              297 AA;
                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 AA
                                                                                                                      1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVDVEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAKA ) OTSUKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1989;
27-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-1990;
                                                                                                                                                                                                                                                                                     28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                         EP407942-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Majima E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
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Matches
                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY24795
ID AAY2
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AC AAY2
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                                                                                                                                                                                                      The present sequence represents a peptide corresponding to amino acids 120-352 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-pecific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. Pl is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of streptokinase encoded by a pST-1 HindIII fragment. Recombinant streptokinase can be produced by culturing bacteria transformed with a high efficiency plasmid contg. the streptokinase gene, amplified by using haemolytic Streptococcus as the template and using inducers based on the streptokinase nucleotide sequence. The recombinant streptokinase is used to treat thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptokinase; recombinant production; haemolytic Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prepn. of streptokinase - useful for treating thrombus diseases
                                                                                                                                 polypeptides which bind streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 20; Length 233; 100.0%; Pred. No. 40; ive 0; Mismatches 0; Indels
                                                                                                                                                                              Disclosure; Page 13; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91599 standard; Protein; 297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 6-8; 24pp; Chinese.
                                                                                                                                                useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYSH-) UNIV SHANGHAI MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94CN-0112106
97US-0055911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-CN00024
                           (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                      Parhami-Seren B, Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100,
les 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase from pST-1
                                                                                                     WPI; 1999-190113/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-358628/46
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SVDVEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVDVEY
18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Gaps

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The sequence was deduced from DNA obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C ) ATCC 10009 or ATCC 9642.

ATCC 9642.

The gene was truncated by 15 codons at the 3' terminal and engineered to add a Met codon prior to codon 16 of the streptokinase CDS. The construct was used to prepare expression vector p6G606 for prodn. of the streptokinase core molecule.

See also AAR12897-R12899 AAR12891-R12893, AAR12895 and AAR12522.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 30; DB 12; Length 369; Best Local Similarity 100.0%; Pred. No. 67; Matches 6; Conservative 0; Mismatches 0; Indels (
                                            Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            streptokinase; thrombolytic agent; myocardial infarction.
                                                                                                           Streptococcus equisimilis ATCC 9542 or ATCC 10009
                                                                                                                                                                                2..369
/label= core streptokinase
/note= "AAs 16-383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptokinase (1-372, Phe 118 deleted).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 88; 115pp; English.
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR10195
ID AAR10195 standard, Protein; 371 AA.
  Truncated Met streptokinase
                                                                                                                                                                                                                                                                                                                                                                    90WO-GB01911
                                                                                                                                                                                                                                                                                                                                                                                                                                      89GB-0027722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-208151/28.
N-PSDB; AAQ12159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA
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                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1989;
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                                                                                                                                                                                                                                                                           WO9109125-A.
                                                                                                                                                                                                                                                                                                                     27-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR10195;
                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a bacterial fibrin-dependent plasminogen activator is useful for the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for a bacterial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least lofold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence represents recombinant streptokinase at least two-fold. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                  Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
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                                          Recombinant streptokinase rSK59-414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 35; Page 65-66; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminally deleted streptokinase
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                                                                                                                                                                                                                                                                                                                                                                                                            97US-0069497
                                                                                                                                                                                                                                                                                                                                                                98WO-US26694
(first entry)
                                                                                                                                                                                                     Streptococcus equisimilis
Synthetic.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-395183/33
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99 SVDVEY 104
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                                                                                                                                                                                                                                                                    WO9931247-A1
                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998;
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26-AUG-1999
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17-SEP-1991
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RESULT 17
AAR12892
ID AAR12
XX
AC AAR12
XX
DT 25-MAJ
DT 17-SE

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Gaps

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256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-6 and AAR10198-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-lys 414) and retaining streptokinase activity. One or more of the amino acids can be replaced by a different amino acid at the same position or it can be deleted. Alternatively, an extra residue can be inserted into the sequence. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in Selectivity and thrombus or myocardial infarction. See also AAQ10230 and AAR10195-R10199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prodn.
                                                                                                             Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic gene encoding streptokinase - scale, high purity of streptokinase used as a thrombolytic agent
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                   streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                           100.0%; Score 30; DB 12; 100.0%; Pred. No. 68;
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100.0%; Pred. No. 68;
tive 0; Mismatches 0;
                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                          AAR10200 standard; Protein; 372 AA
                                                                                                                                                                                                                                                                                                                                          Streptokinase (1-372) derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 59; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-0096830.
89JP-0179432.
89JP-0307957.
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                                                                                                                         Best Local Similarity 100.
Matches 6; Conservative
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1es 6; Conservative
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                                                                                                                                                                                          157 SVDVEY 162
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                                                                                 372 AA;
                                                                                                                                                                1 SVDVEY 6
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11-JUL-1989;
27-NOV~1989;
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                                                                                  Sequence
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                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                            Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and Phe at position 118 being deleted. Alternatively, Phe 118 can be replaced with any other amino acid. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in several with lung thrombus or myocardial infarction. See also AAQ10230 and AAR10196-R10200.
                                                                                                                                              Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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373-Lys 414) and Gln being substituted for Lys at both positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptokinase; thrombolytic agent; myocardial infarction.
                                                                                            Uenoyama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uenoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptokinase (1-372, Gln 256, Gln 257)
                                                                                            Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR10197 standard; Protein; 372 AA.
                                                                                                                                                                                     Claim 8; Page 59; 76pp; English.
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            90JP-0096830.
89JP-0179432.
89JP-0307957.
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89JP-0179432.
89JP-0307957.
                                                                                            Ono K,
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                                                                (SAKA ) OTSUKA PHARM FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                         Ogino K,
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                                                                                                                     WPI; 1991-016179/03
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Sequence 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVDVEY 6
                        11-JUL-1989;
27-NOV-1989;
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11-JUL-1989;
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                                                                                           Majima E,
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Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lyg 414) and Pro residues being inserted next to Lyg at both positions 256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AQ10230, AAR10195-7 and AAR10199-R10200.
                                                                                                                                                                                                                                                                                                                                                                Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 12; Length 374; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptokinase, SKC-2; plasminogen, plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
                streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                               Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Torrens Madrazo IDC, Garcia Ojalvo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY84007 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 59; 76pp; English
                                                                                                                                                                                                      89JP-0179432.
89JP-0307957.
                                                                                                                                                                                                                                                                                               Ono K,
                                                                                                                                                      90EP-0113099
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Best Local Similarity luv...
6, Conservative
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27-NOV-1989;
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                                                                                                                   16-JAN-1991
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                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a mutant protein of the streptokinase SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full-length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De La Fuente Garcia JDJ;
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                                                                                                                                                                                 Streptokinase, SKC-2; plasminogen; plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
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                                                                                                                                                Amino acid sequence of a mutant streptokinase
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                                                                                                              (first entry)
                                                                                                                                                                                                                                                                      Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seralena Menendez A;
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157 SVDVEY 162
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Best Local Similarity
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                                                                                                            03-JUL-2000
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         RESULT 21
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example of a streptokinase derivative which is a combination of two individually claimed modifications. Derivatives between the stability is a show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in spatients with lung thromboly or myocardial infarction. See also AAQ10230, AAR10195-8 and AAR10200.
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 25
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                                                                                                            Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
                                                                                                                                                                                                                                       The present sequence represents a mutant protein of the streptokinase SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full-length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating mycoardial infartion, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ithetic gene encoding streptokinase - scale, high purity prodn. streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                     Disclosure; Page 24-25; 54pp; English.
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89JP-0179432.
89JP-0307957.
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  Seralena Menendez A;
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                                              2000-226041/20
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                                              WPI; 2000-226041,
N-PSDB; AAZ99252
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                                                                                                                                      agents for tre
or C-terminus
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27-NOV-1989;
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AAR10199
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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De La Fuente Garcia JDJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptokinase; SKC-2; plasminogen; plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
      Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 401;
                                                                     Indels
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Query Match
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
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                                                                                                                                                                                                                                                                                                                                                                                AAY84004 standard; Protein; 401 AA.
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Seralena Menendez A;
                                                                                                                                                                                                         134 SVDVEY 139
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                                                                                                                                          1 SVDVEY
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KW Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia; KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; kW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; meurodegenerative disorder; Parkinson's disease; Alzheimer's disease; KW Huntingron's disease; careballar degeneration; cardiovascular disease; femilial amyotrophic lateral sclerosis; atherosclerosis; heart failure; KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial; kw systemic lupus erythematosus; insulin-dependent; diabetes mellitus; kW systemic lupus erythematosus; insulin-dependent; diabetes mellitus; kW wegener's granulomatosus; lisunin-dependent; diabetes mellitus; Socren's syndrome; temporal arthritis; auti-phospholipid syndrome; kW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; kW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; w pancreatitis, Crohn's disease; ulcerative collitis; motor neuron disease; collitis; collitis; motor neuron disease; collitis; motor neuron disease; collitis; collitis; motor neuron disease; collitis; col
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                              Pred. No. 74;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY25020 standard; peptide; 413 AA.
100.08; F1.
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                                                                                                                                                                                                              144 SVDVEY 149
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                     Best Local Similarity
Matches 6, Conserv
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05-DEC-1996;
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reperfusion injury, and hypertensive heart disease), immune disease (e.g. theumatoid arthritis, systemic lupus erythematosus, insulin-dependent, diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema nodosum, Sjogren's pernicious anaemia, dermatomyositis, enythema nodosum, Sjogren's syndrome, temporal arthritis, mysathenia gravis, wegener's granulomatosis, glomerulomephritis, anti-phospholipid syndrome, and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia, arconas, myelomas, carcinomas, nelanoma, cancers of the beart, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury, realial schemia, spinal cord ischemia and/or insult (e.g. niver toxicity, retinal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia, spinal cord ischemia and/or insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxious substances), macular degeneration, cateract formation, pancreatitis, Crohn's disease, culcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemically-induced reperfusion, and therapeutics such as clozapine, AZT and anthracyclines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 20; Length 413; 100.0%; Pred. No. 76; 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a mutant streptokinase.
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Best Local Similarity 100...
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Streptokinase; cell death; apoptosis; necrosis; nootropic;
neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;
antiinflammatory; antiarthritic; antichematic; cardiant;
which antiarther antidabetic; immunosuppressive; anti-HIV;
dermatological; antidiabetic; immunosuppressive; anti-HIV;
whithson's disease; altheimer's disease; huntington's disease;
Parkinson's disease; haltheimer's disease; huntington's disease;
wherebellar degeneration; neoplastic disease; huntington's disease;
whithson's disease; heart failure; atherosclerosis;
oradiovascular disease; heart failure; atherosclerosis;
whocardial reperfusion injury; immune disease; autoimmune disease;
wystemic lupus erythematosus; diabetes mellitus; pernicious anemia;
wystemic lupus diseases; viral diseases; macular degeneration;
whelodegenerative diseases; viral diseases; macular degeneration;
who disease; aging.
SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
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                                                                                                                                                                                                                                                        100.0%; Score 30; DB 21; Length 413; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                          0; Indels
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96US-0759599.
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Best Local Similarity 100.
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                                                                                                                                                                                                                       413 AA
                                                                                                                                                                                                                                                                                                                               1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1995;
05-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-FEB-2002.
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80012;
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80012
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Disclosure, Fig 3, 18pp, English

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antimifiammatory, antiparkinsonian, anticonvulsant, cytostatic, antimifiammatory, antiathritic, antirheumatic, cardiant, consistences of the invention are useful computations of antiulcer, antidabetic, antianaemic, virucide, ophthalmological, antidabetic, antidaemic, virucides of the invention are useful for treating comprising peptides of the invention are useful for treating concerning diseases (e.g. harkinson's, Alzheimer's, Huntington's disease and cerebellar degeneration) neoplastic diseaders including cancer, inflammatory disorders (e.g. arthritis; inflammatory joint diseases and cardiovascular diseases (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune cystemic lupus erythematosus, diabetes mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases, ulcerative colitis, cataractes, and crementaled aging. The current sequence represents a representative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atherosclerosis; myocardial infarction; immune disease; carcinoma; rheumatoid arthritis; mopplastic disorder; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; arthritis; inflammatory induced cell damage; motor neuron disease; physical insult; severe shock; ischaemia; reperfusion injury; hepatitis; cell dath associated procedure; spinal cord reperfusion injury; toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease; Guillain-Bare syndrome; bypass surgery; myocardial ischaemia; chemotherapp; viral disease; viral encephalitis; infectious disease; bacterial disease; prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging; oxidative stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 18mer_peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2. This is SEQ ID NO 5 as shown
in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell death ameliorating peptide. Specifically claimed in claim 2"
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/label= 6mer_peptide_#1
/note= "Cell_death_ameli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Representative streptokinase sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156..173
/label= 18mer_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG74199 standard, Protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             streptokinase amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .56..171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG74199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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1 SVDVEY 6

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The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliorating cell death, its derivative or analogue, comprising a sequence Val-Asp-Val, where the peptide is in a suitable pharmaceutical carrier or diluent. The pharmaceutical composition comprising the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's catheroscleropis and myocardial infarction; immune disease e.g. AIDS and alsease and Alzheimer's disease; cardiovascular disease e.g. AIDS and atheroscleropis and myocardial infarction; immune disease e.g. AIDS and inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and severe shock; inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and severe shock; inchaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord certical insult e.g. invertoxicity and pulmonary corticity, spinal cord disease e.g. motor neuron disease and Guillain-Bare syndrome; procedures associated with cell death e.g. bypass surgery and chemotherapy; viral disease e.g. hepatitis and viral encephalitis; cohurs disease; infectious diseases e.g. hepatitis and viral encephalitis; uncertaine colitis, accelerated aging and oxidative stress in a warm-blooded animal. The present sequence represents the amino acid sequence of a representative streptoxinase from which the cell death ameliorating peptides are produced.
/note= "Cell death ameliorating peptide. Specifically claimed in claim 2. This is SEQ ID NO 5 as shown on page 8"
                                                       156..176
/label= Fraction 13 peptide
/label= Fraction 13 peptide
/note= "Cell death ameliorating peptide. Specifically
/noteind in claim 2"
                                                                                                                                                                                                                                                                                      299..318
/label= Fraction 12 peptide
/note= "Cell death ameliorating peptide. Specifically
oralimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                     /label= 6mer_peptide #2
/note= "Cell_death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                               /label= 11mer peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 3; 19pp; English
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99US-0294457.
96US-0759599.
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                                                                                                                                   299..304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krystal G, Rabkin SW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-246673/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 AA;
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19-APR-1999;
05-DEC-1996;
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                                                                                                                                                                                                                                                                                          Peptide
                                                           Peptide
                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                            Synthetic gene encoding streptokinase - scale, high purity prodn of streptokinase used as a thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents in patients with lung thrombus or myocardial infarction.
See also AAR10195-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 12; Length 414; 100.0%; Pred. No. 76; of Mismatches 0; Indels (
                                                                                                                                      streptokinase; thrombolytic agent; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasminogen activator; coronary thrombosis; ATCC-9542.
                                                                                                                                                                                                                                                                                                          Uenoyama
                                                                                                                 Streptokinase encoded by synthetic gene
                                                                                                                                                                                                                                                                                                          Sakata Y,
                                                     AAR10194 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR20202 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 51; 76pp; English
                                                                                                                                                                                                                                            90JP-0096830.
89JP-0179432.
                                                                                                                                                                                                                         90EP-0113099.
                                                                                                                                                                                                                                                                                                         Ono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.equisimilis streptokinase.
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                                                                                                                                                                                                                                                                                     (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
                                                                                                                                                                                                                                                                                                         Majima E, Ogino K,
                                                                                                                                                                                                                                                                                                                              WPI; 1991-016179/03
156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ10230
                                                                                                                                                                                                                        09-JUL-1990;
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                                                                                            28-MAR-1991
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21-APR-1992
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                                                                                                                                                                              EP407942-A.
                                                                                                                                                           Synthetic.
                                                                       AAR10194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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100.0%; Score 30; DB 24; Length 413; 100.0%; Pred. No. 76; tive 0; Mismatches 0; Indels (

Conservative

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93WO-US09502.
                              92US-0956692.
                                       93US-0128299.
                                                          (GEHO ) GEN HOSPITAL CORP.
                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
                                                                                                           WPI; 1994-135561/16.
                                                                                                                                                                                                                                                                                                                                            SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-395183/33
                                                                                                                                                                                                                                                              414 AA;
                                                                                                                                                                                                                                                                                                                         1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX80492
         05-OCT-1993;
                             05-OCT-1992;
                                       29-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9931247-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1999.
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                             157
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY24794;
                                                                                        Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed GL;
                                                                                                                                                                                                                                                                                                                                                                           RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                   AAY24794
ID AAY
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                                                                                                                                                                                                               The SKC-2 gene was isolated from S.equisimilis type C by gene amplification from the synthetic primers SK1, SK2 and SK3 (see AAQ20666-8). The SKC-2 gene was inserted into yeast expression vector PS-7 for extracellular expression of streptokinase and into pNAO for intracellular expression in yeast. For expression in bacteria, the SKC-2 gene was inserted in plasmid pEKG3, between a trp promoter and a T4 terminator.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                       Streptokinase C-2 gene from S.equisimilis type C - plasmids and transformants for large scale intra- and extracellular expression of SKC-2 useful in thrombolytic agents
                                                                                    Hidalgo AP, Doce RS, Marrero LFH;
Munoz EAM, Martinez WB, Somavilla MC;
Martinez LSH;
                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 13; Length 414; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptokinase; SK; Streptococcus equisimilis; plasminogen; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                (INGG-) CENT ING GENETICA & BIOTECNOLOGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "claim 3, see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244..352
/note= "claim 2, see
1..352
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/note= "claim 3, see
244..414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "claim 3, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                Claim 13; Page 14; 28pp; English
                         91AU-0078101.
                                             90CU-0000090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                    Chaplen RR,
Ramirez AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus equisimilis.
                                                                                                       Garcia J,
                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
                                                                                                                           WPI; 1992-024716/04.
                                                                                                                                                                                                                                                                                                                                                                                     SVDVEY 162
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                            414 AA;
                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY 6
                                                                                                                                    N-PSDB; AAQ20665
                                                                                   Garcia MPE, Ch
Collazo PR, Ra
Fernandez AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase
                        31-MAY-1991;
                                             23-MAY-1990;
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16-NOV-1994
       28-NOV-1991
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                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                      Nucleic acid comprising a sequence encoding amino acids 14-414 of streptokinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 120-352 or 244-414.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Length 414;
DNA encoding a polypeptide which binds to plasminogen and corresponds to region of streptokinase - useful to detect plasminogen in a sample and to treat myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus equisimilis native streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 76; Matches 6; Conservative 0; Mismatches
                                                                                                                                          Disclosure; Page 40-41; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 30; Page 60-61; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24794 standard; Protein; 414 AA.
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induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence represents native streptokinase at least two-fold. The present
   present invention describes an isolated bacterial protein that
$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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1 SVDVEY 6 Sequence

/ Match 100.0%; Score 30; DB 20; Length 414; Local Similarity 100.0%; Pred. No. 76; of Conservative 0; Mismatches 0; Indels (SVDVEY 162 157 Query Match Matches ठ 셤

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Gaps

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AAY01556 standard; peptide; 414 AA.

(first entry) 18-JUN-1999 AAY01556;

Native streptokinase protein sequence.

Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis, rheumatic fever

Streptococcus equisimilis

WO9908698-A1

25-FEB-1999.

98WO-US17114 18-AUG-1998;

97US-0055911 18-AUG-1997;

(GEHO) GEN HOSPITAL CORP. (HARD) HARVARD COLLEGE.

Parhami-Seren B, Reed GL;

WPI; 1999~190113/16.

New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy

Disclosure, Page 12; 44pp; English.

The present sequence represents a native streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also

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414

Seguence

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                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus equisimilis H46A, streptokinase, mutant; fibrinolytic; plaama clot, hydrolysis, haemolytic Streptococcus; plasmingen; plasmin, serine protease; fibrin; blood clot; thrombolytic; vascular thrombolytic; symptom; acute myocardial infarction;
describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. P1 is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic
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                                                                                                                            20; Length 414;
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                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus equisimilis native streptokinase.
                                                                                                                           Score 30; DB 2
Pred. No. 76;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 7-10; 17pp; English.
                                                                                                                                                                                                                                                                                                      AAW94664 standard, Protein, 414 AA.
                                                                                                                         100.0%; Sc
100.0%; Pr
ive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0568393
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrinolysis; resistance.
                                                                                                                                                            6; Conservative
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                                                                                                                                                                                                                       157 SVDVEY 162
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                                                                                                                        Query Match
Best Local Similarity
                                                                                             414 AA;
                                                                                                                                                                                         1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombolytic agent
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                                                                                               Seguence
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Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunogl bulin; thexapeutic; streptokinase.

Streptococcus equisimilis.

WO9852976-A1.

26-NOV-1998

Streptokinase (SK) protein sequence.

03-MAR-1999

AAW86143;

AAW86143 standard; Protein; 414 AA

RESULT 37 AAW86143

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the ProS8-LyaS9-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence is mutant SK K59E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPIg) to plasmin (HPIm), which is a serine protease able to catalyse the agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen.
                                               Gaps
                                                                                                                                                                                                                                                                                             Streptococcus equisimilis H46A, streptokinase, mutant; fibrinolytic; plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant streptokinase polypeptide - useful as plasmin-resistant thrombolytic agent
               100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                 Streptococcus equisimilis mutant streptokinase K59E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by ACC"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                             AAW94665 standard; Protein; 414 AA.
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Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                        fibrinolysis; resistance.
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Best Local Similarity 100.
Matches 6; Conservative
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N-PSDB; AAX16633.
                                                                                                    SVDVEY 162
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                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                               RESULT 36
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Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species

98GB-0007751. 97GB-0010480. 97GB-0016197. 97GB-0025270. 97US-0067235.

21-MAY-1997; 31-JUL-1997; 28-NOV-1997;

02-DEC-1997;

(BIOV-) BIOVATION LTD

WPI; 1999-045301/04

Carr FJ;

98WO-GB01473

21-MAY-1998; 14-APR-1998;

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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein, (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species, and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW86144 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Fig 28; 77pp; English.
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AAW86144
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AC AAW86:
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Gaps

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100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; ive 0; Mismatches 0; Indels 0

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invention relates to a method for the production of non-immunogenic
                          Non-immunogenic, epitope, T-cell; immunogenicity; immune system; SK;
immunogl bulin; therapeutic; streptokinase; de-immunised.
                                                                                                                                                                                                                               Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
         De-immunised streptokinase (SK) protein sequence
                                                                                                                                                                                                                                                                        Example 6; Fig 29; 77pp; English
                                                                                                                           98GB-0007751.
97GB-0010480.
97GB-0016197.
97GB-0025270.
                                                                                                           98WO-GB01473
                                                     Streptococcus equisimilis
                                                                                                                                                                                (BIOV-) BIOVATION LTD
                                                                                                                                                                                                                   WPI; 1999-045301/04.
                                                                                                                                                                                                                                                                                                                                                                                                                       414 AA;
                                                                      WO9852976-A1
                                                                                                                                                              02-DEC-1997;
                                                                                                                                   21-MAY-1997;
31-JUL-1997;
                                                                                       26-NOV-1998
                                                                                                                                                      28-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                   Carr FJ;
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proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cell epitopes) of the given species, and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunospanicity of the protein when exposed to the immunospanicity of the protein when exposed to the immunospanic the pays a method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The immunoglobulins or therapeutic protein of the immunoglobulins or therapeutic protein the products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of a de-immunised SK protein molecule.

. 0 Query Match
Best Local Similarity 100.0%; Pred. No. 76; Length 414;
Matches 6; Conservative 0; Mismatches 0; Indels 9 1 SVDVEY ð

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Gaps

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157 SVDVEY 162 g

Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; fibronectin.

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This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between streptokinase (SK), which are deadled fusion between the streptokinase (SK), which are deadled fusion between the streptokinase (SK), which are deadled fusion between the streptokinase (SK), which are from fibrin binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the bablity to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable and pronounced duration, or lag, after exposure of the PA to a suitable candiovascular disorders. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action that man of plasmin fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation cencountered during clinical use of streptokinase.
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                    Sundaram V;
                                                                                                                                                                                                                                                                                                                      Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin
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                                                                                                                                                                                                    Rajogopal K, Nihalani D,
                                                                                                                                                           (COUL ) CSIR COUNCIL SCI IND RES
                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 3; 58pp; English
                                                                              99EP-0310541
                                                                                                                      98IN-0003825
                                                                                                                                                                                                  Kumar R, Roy C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 10v...
6; Conservative
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N-PSDB; AAA37633.
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EP1024192-A2
                                                                              23-DEC-1999;
                                                                                                                      24-DEC-1998;
                                       02-AUG-2000,
                                                                                                                                                                                                Sahni G,
Yadav M;
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(first entry) 25-SEP-2000 AAB01295;

AAB01295 standard; protein; 414 AA.

RESULT 40 AAB01295 Wild type streptokinase from Streptococcus equisimilis.

Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug; vaccine; carriter; diagnosis; therapy; complement; C3; C5; CVF; plaeminogen; streptokinase; fibrin; blood clot; thrombolysis; plaemin; myocardial infarction.

Streptococcus equisimilis

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Proteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for the producing a protein with an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive drugs to its active form within a living organism. The method can be needed active or introduced within the living organism in order to alter the bid distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a therapeutic or a diagnostic agent. Streptowkinase is produced by certain strains of beta-haemolytic streptococci. The protein has no inherent enzymatic activity but has considerable clinical importance of inherent enzymatic activity but has considerable clinical importance of inherent is sativation to plasmin and thereby promoting the effective thrombolytic agent in the treatment of croonary thrombosis, or improving survival and preserving left ventricular function following production of neutralising antibodies in humans generally limits the protein to a single use. The new method could provide a longer therapeutic use for streptokinase. The altered streptokinase sequence is singiven in AAB01296. See GENDESEQ records AAB01289-B01302.
                                                                                                                                                                                                                                                                                           Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 21; Length 414; 100.0%; Pred. No. 76;
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                                                                           99WO-GB04119
                                                                                                                98GB-0026925
99GB-0002139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                         (BIOV-) BIOVATION LTD.
                                                                                                                                                                                                                 Carr FJ, Adair FS,
                                                                                                                                                                                                                                                      WPI; 2000-423372/36.
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WO200034317-A2
                                                                                                              08-DEC-1998;
02-FEB-1999;
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                                    15-JUN-2000
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AAB01296 standard; protein; 414 AA 25-SEP-2000 (first entry) AAB01296;

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Gaps

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Altered streptokinase from Streptococcus equisimilis.

Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug; vaccine; carrier; diagnosis; therapy; complement; C3; C5; CVF; plasminogen; streptokinase; fibrin; blood clot; thrombolysis;

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Proteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell ceptopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for the immune system of another organism. The method can be used for the producing a protein with an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive drugs to its active form within a living organism, a vaccine, a protein used as a carrier of other molecule or a protein which binds to other molecules within or introduced within the living organism in order to alter the bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medianosis, dispnosis and in manufacture of a terminatic of beca-haemolytic streptochiase is produced by certain strains of beca-haemolytic streptochiase is produced by cortein the activity but has considerable clinical importance of inherent enzymatic activity but has considerable clinical importance of inherent enzymatic activity but has considerable clinical importance of insolution to efficiently bind human plasminogen, the dissolution of fibrin filaments in blood clots Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, importance of improving survival and preserving left ventricular function following mycardial infarction. The native protein is immunogenic and the protein to a production of neutralising antibodies in humans generally limits the coronary manner of coronary humans generally limits the protein to a neutralish was manner when a coronary humans generally limits the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
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                                                                                                                                                                                                                                                                                                                                                    Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB74940 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                  Hamilton AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 6; 42pp; English.
  plasmin; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the altered streptokinase.
                                                                                                                                                                                               99WO-GB04119
                                                                                                                                                                                                                                       98GB-0026925
99GB-0002139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.00
Enhea 6; Conservative
                                                                Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                     (BIOV-) BIOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                  Carr FJ, Adair FS,
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-423372/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVDVEY 6
                                                                                                          WO200034317-A2
                                                                                                                                                                                                                                     08-DEC-1998;
02-FEB-1999;
                                                                                                                                                                                             08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001
                                                                                                                                                  15-JUN-2000
                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB74940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB74940
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Streptococcus plasminogen activator, streptokinase

(first entry)

13-SEP-2000

AAY99593;

AAY99593 standard; protein; 415 AA.

43 AAY99593 Plasminogen activator; cardiant; thrombolytic; heart attack; stroke; blood clotting disorder.

Streptococcus ap. WO200032759-A1. (OKLA-) OKLAHOMA MEDICAL RES FOUND.

02-DEC-1998; 06-MAY-1999;

Zhang XC, Tang JJN;

Lin X,

.16660SU-OW66 98US-0110588.

08-JUN-2000.

us-09-919-703-1.open.rag

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The present invention describes a method to create mutants of streptokinase (SK) which become more resistant to hydrolytic inactivation by human plasmin (HPIM) and more effective in activation of chuman plasmin (HPIM) and more effective in activation of chuman plasmin (HPIM) than the native SK that is commercially available. The novel HPIM hydrolysis resistant SK can be created by the near the peptide bonds that are hydrolysed by HPIM. The mutant SK can be used to form HPID and native SK and could be used as a thrombolytic agent. The mutant SK sequence could be coupled with other proteins to form fusion proteins and improve the fibrinolytic activity of the fusion proteins. Some truncated SKs such as SKIG-378) could activate HPIG as efficiently as native SK. The truncated SKs comprising the modification of ProS8-LysS-Ser60-Lys61 to other amino acids would have a better thrombolytic activity than the corresponding native truncated SK. Since LysS-Ser60 is among the few peptide bonds which are cleaved in the early reaction with HPIM and the NH2-terminal peptide chain of 116-LysS9 is essential in stabilising the structure of SK, the mutation at/or near by the peptide bond and might improve the stability of the hydrolysis of the peptide bond and might improve the stability of streptokinase (KSBE) given in the present sequence represents the mutant streptokinase (KSBE) given in the present invention.

N.B. The present sequence corresponds to the indexers best interpretation or print.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of novel streptokinase mutants as improved thrombolytic
                                                                                                                                                                                                                      Misc-difference 370
/label= unknown
/note= "given as being encoded by NRN due to poor
quality text"
                                                                                                                                                                                                   /note= "given as being encoded by NNN due to poor
quality text"
                                    Streptokinase; mutant; human; plasmin; plasminogen; thrombolytic.
                                                                                                                                           note= "Lys in wild type sequence"
Mutant streptokinase protein sequence K59E.
                                                                                                           Location/Qualifiers
                                                                                                                                                                                   'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1; 4pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                              95TW-0107238.
                                                                                                                                                                                                                                                                                                                                                                                                          95TW-0107238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NASC-) NAT SCI COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-326604/34.
                                                                                                                                                                Misc-difference 127
                                                                                                                              Misc-difference 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF82144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu H, Shr G;
                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-1995;
                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                     01-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agents
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The present sequence is streptokinase, a single-peptide secretory protein which is produced by various strains of haemolytic Streptococcus. Streptokinase forms a tight binding complex with human plasminogen, causing the spontaneous conversion of plasminogen to its active form, plasmin. Plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Plasmin is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen activators regulate plasminogen expression either by forming a binding complex, as in the case of streptokinase, or by hydrolysing a peptide bond in plasminogen to convert it to plasmin. Review of sequence homologies of several plasminogen activators and chymotrypsin has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length chuman plasminogen. Novel plasminogen activators have been made based upon chuman plasminogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thresholvers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or treating blood clotting disorders such as heart attack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 29-31; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY50870 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 44
AAY50870
ID AAY50
XX
AC AAY50
XX
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Gaps

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Query Match
Best Local Similarity 100.0%; Score 30; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels

157 SVDVEY 162

g ठ

1 SVDVEY 6

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Streptokinase produced using E.coli transformed with a recombinant streptokinase vector can be isolated for use as a thrombolytic agent to facilitate the in vivo lysis or dissolution of blood clots. The vector is esp. a plasmid obtd. from E.coli, esp. plasmid pBR 322. Recombinant plasmid pMF1 as defined by a restriction endonuclease map is claimed. Escherichia coli HB 101 harbouring plasmid pMF1 is deposited as ATCC 39613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptokinase A; recombinant phage; thrombolytic agent; plasminogen;
                                                                                                                                                                                                                                       Streptokinase prodn. - by cultivating Escherichia coli ATCC 39613 contg. recombinant plasmid pMF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High yield streptokinase A prodn. from infected bacteria - contg.
recombinant phage including gene from Streptococcus, useful as
thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 30; DB 6; Length 440; 100.0%; Pred. No. 82; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptokinase A from Streptococcus pyogenes SF130/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR06378 standard, protein, 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEAK ) AKAD WISSENSCHAFTEN DDR.
                                                                                      (PHIP ) PHILLIPS PETROLEUM CO. (UYOK-) UNIV OF OKLAHOMA.
                                                                                                                                                                                                                                                                                            Example, Fig 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 2; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malke H;
                84US-0585417.
83DD-0255523.
83DD-0255235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88DD-0321532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes.
                                                                                                                                              Perretti JJ, Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (nbdated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walter F, Siegel M,
                                                                                                                                                                                WPI; 1985-135032/23.
N-PSDB; AAN50493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-247328/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ05604.
                02-MAR-1984;
10-OCT-1983;
10-OCT-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
20-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06378;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel thrombolytic agent comprising streptokinase where at least one nonessential portion has been modified. The invention also describes a method of forming a thrombolytic agent comprising determining a nonessential portion of streptokinase and modifying the nonessential portion to render the resulting protein less antigenic. The modified streptokinase is used to treat blood clot disorders, such as heart attacks. The modified streptokinase has less antigenicity than streptokinase but is still able to complex plasminogen and lead to plasminogen activation. Modified streptokinase with the nonessential portions removed or truncated simplify the molecule. Such smaller proteins are cheaper and easier to produce. This sequence represents a fragment of a Streptococcus sp. streptokinase protein which is used in the description of the method of the invention.
                                                                     Thrombolytic agent; streptokinase; antigenic; blood clot; heart attack;
                                                                                                                                                                                                                                                                                                                                                                                                                    New thrombolytic agents derived from modified humanized streptokinase, useful for treating blood clot disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded by skc streptokinase gene on the 2.5\mathrm{kb} PstI produced pMF1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ົວ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus equisimilis strain H46A (serological group
                                   Streptococcus sp. streptokinase protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzyme; thrombolytic agent; blood clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 48-49; 55pp; English
                                                                                                                                                                                                                                                                                                         (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP50620 standard; Protein; 440 AA
                                                                                                                                                                                                                                                                     98US-0084392.
                                                                                                                                                                                                                                                                                                                                              Lin X, Tang JJN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84AU-0033859
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Best Local Similarity 100.vv
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 AA
                                                                                                                            Homo sapiens
                                                                                                                                                            WO9957251-A2.
                                                                                                                                                                                                                                                                       06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-1984;
24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-1991
                                                                                                                                                                                               11-NOV-11999
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                                                                                                                                                                                                                                                                                                                                            Zhang XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local Similarity
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       Lambda L47.1 is ligated with genomic DNA from S. pyogenes SF130/13 and the resultant product used to transform bacteria. Infected cells are cultured in liq. medium contg. assimilable C and N sources, and streptokinase A is isolated from the cell lysate. The infected cells provide the protein in high yields, i.e. 1000 U/ml compared to 80 U/m, for the donor strain. The protein activates the autocatalytic conversion of human plaminogen to human plasmin, so is potentially useful as a thronbolytic (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pWN1 (contg. the streptokinase G gene ) is ligated with pUC19 and the resultant product used to transform bacteria. Infected cells are cultured in 1iq. medium contg. assimilable C and N sources, and streptokinase G is isolated from the cell lysate.

The infected cells provide the protein in high yields, i.e. 600 U/ml which is 1.5-2 times that for the donor strain. The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thronbolytic agent. See also DD-276634 (AAQ05664).

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High yield streptokinase G prodn. from recombinant cells -
transformed with plasmid contg. gene from Streptococcus, useful
as thrombolytic agent
                                                                                                                                                                 ö
                                                                                                                                           100.0%; Score 30; DB 11; Length 440; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                  Streptokinase G protein from Streptococcus pyogenes G19908.
                                                                                                                                                                                                                                                                                                                                                    Streptokinase G; thrombolytic agent; plasminogen; plasmin;
                                                                                                                                                                Indels
                                                                                                                                                                .
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                           AAR06377 standard; protein; 440 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 88DD-0321531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88DD-0321531.
                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siegel M,
                                                                                                                                                                                                                                                                                                                                                                 recombinant plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-247327/33.
                                                                                                                                                                                                        183 SVDVEY 188
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                        440 AA;
                                                                                                                                                                                    φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 AA
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                                                                                                                                                                                    1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-1988;
                                                                                                                                                                                                                                                                                                  25-MAR-2003
20-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                        DD276693-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walter F,
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                               AAR06377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                Matches
                                                                                                                                                                                                                                       RESULT 47
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the active agents are released specifically at the place where clot
formation is occurring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
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82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase.
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also R12887, R12888, R12891-R12894, R12885 and R12522 (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis ATCC 9542 or ATCC 100009
                                                    ö
100.0%; Score 30; DB 11;
11arity 100.0%; Pred. No. 82;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27..440
/label= mature streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..26
/label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 80; 115pp; English
                                                                                                                                                                                                                                                                                     AAR12889 standard; Protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRBI-) BRITISH BIO-TECHNOLOGY LTD
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-208151/28.
N-PSDB; AAQ12156.
                                                                                                                                                         183 SVDVEY 188
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Best Local Similarity
                                                                                                       9
                                                                                                    1 SVDVBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1990;
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17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                     AAR12889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                   RESULT 48
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AAR12885 standard; Protein; 483 AA

RESULT 50 4AR12885

183 SVDVEY 188

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 543 sequences (31), given in the specification. The proteins have antibacterial and antiinflammatory activity. [1], nucleic acids encoding (1), ABN6604-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is are used to detecraine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningits. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity contractors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C;
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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masignani V, Margarit Ros YI,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide SEQ ID NO 8298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3946; 4525pp; English.
                                                                                                                                                                                                                                                                    ABP29561 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001; 2001WO-GB04789.
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Best Local Similarity 100.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-352536/38.
N-PSDB; ABN70192.
                                                                                                                  183 SVDVEY 188
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                                                          1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                            ABP29561;
                                                                                                                                                                                                      ABP29561
ID ABP29561
XX AC ABP29
XX Strep
CC Strep
Matches
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The protein is a recombinant product of a gene fusion construct.

The sequence of the synthetic hirudin HV-1 genes was designed based on the published manho acid sequence (bodt J., et al FEBS Letters 165 180 (1984)). The sequence of streptokinase was obtd.

From PCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9942. The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two sequences were used to construct an expression vector in which the hirudin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are cleased specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12894 and AAR12522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                  Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis.
                                                                                                                                                                                                                                                                        note= "factor Xa cleavage site"
                                                                                      Factor Xa-cleavable hirudin-IEGR-streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dawson KM, Hunter MG, Czapleswski LG;
                                                                                                                                                                                                                                                                                       70..483
/label= streptokinase
                                                                                                                                                                                                                 1..65
/label= hirudin HV-1
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 96; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                                                                                                                                                              56..69
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                 90WO-GB01911.
                                                                                                                                                                                                                                                                                                                                                                                                                              90WO-GB01911
                                                                                                                                                                                                                                                                                                                                                                                                                                             89GB-0027722
                                          (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ12162
                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1989;
                                        25-MAR-2003
17-SEP-1991
                                                                                                                                                                                                                                                                                                                                     WO9109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                   27-JUN-1991
                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
            AAR12885;
                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                           Peptide
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Gaps

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100.0%; Score 30; DB 23; Length 440; 100.0%; Pred. No. 82; 1. Indels 1. Inde

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Search completed: January 20, 2004, 13:56:15 Job time : 43 secs දු පු

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GenCore version 5.1.6
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| OM protein - protein search, using sw model | . January 20, 2004, 13:56:57; Search time 33 Seconds (without alignments) 37.178 Million cell updates/sec | US-09-919-703-1 t score: 30 ce: 1 SVDVEY 6 | g table: вLOSUM62 Gapop 10.0 , Gapext 0.5 | ed: 762491 seqs, 204481190 residues |
|---------------------------------------------|-----------------------------------------------------------------------------------------------------------|--------------------------------------------------|----------------------------------------------|-------------------------------------|
| OM protein - p | Run on: | Title: Perfect score: Sequence: | Scoring table: | Searched: |

Total number of hits satisfying chosen parameters: 762491 Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/DCT_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_DEW PUBL.pep:*

3: /cgn2_6/ptodata/1/pubpaa/DCT_DEW PUBL.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | Description | Sequence 1, Appli | Sequence 5, Appli | Sequence 6, Appli | 7 | 73 | 7 | | Sequence 253, App | | | | ς, | 9 | 7 | Sequence 12, Appl |
|-----------|-------|-------------------------|-------------------|-------------------|-------------------|-----------------|------------------|-----------------|-------------------|-------------------|------------------|--------------------|--------------------|-----------------|-----------------|------------------|-------------------|
| SUMMARIES | | QI | US-09-919-703-1 | US-09-919-703-5 | US-09-919-703-6 | US-09-919-703-7 | US-09-919-703-12 | US-09-940-235-2 | US-10-300-215-252 | US-10-300-215-253 | US-09-862-027-25 | US-10-369-493-5723 | US-10-369-493-6887 | US-09-919-703-3 | US-09-992-807-6 | US-10-209-967-14 | US-10-193-896-12 |
| | | | 10 | 10 | 10 | 10 | 10 | 11 | 12 | 12 | 10 | 12 | 12 | 10 | 10 | 12 | 16 |
| | | wery Watch Length DB | 9 | 16 | 20 | 21 | 413 | 414 | 414 | 414 | 891 | 1207 | 629 | 9 | 355 | 391 | 496 |
| | æ (| Match | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 96.7 | 93.3 | 0.06 | 90.06 | 90.0 | 90.0 |
| | | Score | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 29 | 28 | 27 | 27 | 27 | 27 |
| | 1,000 | No. | н | 7 | 3 | 4 | ស | φ | 7 | 89 | 6 | 10 | 11 | 12 | 13 | 14 | 15 |

| equence 14, equence 25, equence 25, equence 26, equence 14, equence 138 equence 138, equence 41, A quence 41, | Sequence 15.38 Sequence 22955 Sequence 12808 Sequence 1049. Sequence 1147. | equence 2919, equence 11, A equence 21, A equence 21, Ap quence 13170, equence 20, A equence 20, A | equence 3395 equence 4017 equence 2017 equence 281, equence 61, equence 55, equence 56, equence 56, equence 56, equence 60, equence 60, equence 60, equence 60, equence 60, | quence 1078, quence 2612, quence 18531 quence 1983, quence 10953, quence 11913 quence 21430 quence 21430 quence 5078, quence 5078, quence 14987, quence 4287, |
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| US-09-799-629- US-09-927-315- US-10-246-785- US-10-179-373- US-10-035-045- US-10-035-045- US-10-193-477- US-09-737-149-4 | US-10-369-493- US-10-369-493- US-10-369-493- US-10-156-761- US-10-269-762- US-10-369-493- US-10-369-493- | US-103-103-103-103-103-103-103-103-103-103 | US-10-128-714-339 US-10-128-714-839 US-10-369-493-229 US-10-369-493-229 US-10-369-528-54 US-10-360-522-54 US-10-360-522-55 US-10-360-522-56 US-10-360-522-56 US-10-360-522-56 US-10-360-522-56 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US-10-360-522-60 US | US-10-369-493-1 US-10-104-104-107-2 US-10-369-493-1 US-10-369-493-1 US-10-369-493-1 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-2 US-10-369-493-1 US-10-369-493-1 US-10-369-493-1 |
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ALIGNMENTS

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RESULT 1
US-09-919-703-1
US-09-919-703-1
Sequence 1, Application US/09919703
Setent No. US20020165129A1
GENERAL INFORMATION:
FAPELICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
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Gaps
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                                                                                                                                                                                                                                                                                                                                            Length 20;
Sequence 7, Application US/09919703

Patent No. US20020165129A1

GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/00304
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US/09/919,703
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1999-04-19
PRIOR PELING DATE: 1995-12-05
PRIOR PAPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1955-12-06
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7

LENGTH: 21
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Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
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Patent No. US20202165129A1
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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US-09-919-703-12
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 TITLE OF INVENTION: Cell Death
CURRENT APPLICATION NUMBER: US09919,703
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR PILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR PILING DATE: 1995-12-05
PRIOR PILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FaetSEQ for Windows Version 4.0
SENGTH: 6
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                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic polypeptide
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Patent No. US20020165129A1
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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US-09-919-703-5
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Sequence 252, Application US/10300215
Publication No. US20030153043A1
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Sequence 2, Application US/09940235;
Publication No. US2003005921A1
GENERAL INFORMATION:
APPLICANT: Rumar, Rajesh
APPLICANT: Rajespal, Kammara
APPLICANT: Rajespal, Kammara
APPLICANT: Albaland, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Nihaland, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Sandaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Sundaram, Vasudha
APPLICANT: Nihaland, Deepak
TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1998-12-24
CURRENT APPLICATION NUMBER: 09/471,349
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
TITLE OF INVENTION: Cell Death
TITLE OF INVENTION: Cell Death
CURRENT PILIS SO216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT PILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 414
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RESULT 7 US-10-300-215-252

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GENERAL INFORMATION: USJOUGHISOUGHER
APPLICANT: CARR, Francis Joseph
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS
FILE REFERENCE: MRR-104-Con.1
CURRENT APPLICATION NUMBER: US 09/438,136
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-62-1
PRIOR APPLICATION NUMBER: GB 9710480.6
PRIOR APPLICATION NUMBER: GB 971047.0
PRIOR PILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-20
NUMBER OF SEQ ID NOS: 254
SOTTWARE: FASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 252
LENGTH: 414
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Publication No. US200301530431
GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: AMAILTON, Anita Anne
APPLICANT: AMAILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
FILE REFERENCE: MER-104-Con.1
CURRENT APPLICATION NUMBER: US/10/300,215
FRICK FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1998-05-21
FRIOR FILING DATE: 1997-07-31
FRIOR FILING DATE: 1998-04-14
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US-10-300-215-252
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Best Local Similarity 100.
Matches 6; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6887
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j Sequence 3, Application US/09919703

j Sequence 3, Application US/09919703

j Sequence 3, Application US/09919703

j Renet No. US20020165129A1

j GENERAL INFORMATION:

APPLICANT: Krystal, Gerald

TITLE OF INVENTION: Peptides and Their Use to Ameliorate

TITLE OF INVENTION: Peptides and Their Use to Ameliorate

TITLE REFERENCE: 50216/003004

CURRENT APPLICATION WINBER: US/09/919,703

CURRENT FILING DATE: 1099-04-19

PRIOR PAPLICATION NUMBER: US 09/294,457

PRIOR PLICATION NUMBER: US 09/294,457

PRIOR PLICATION NUMBER: US 09/294,57

PRIOR PLICATION NUMBER: US 60/008,233

PRIOR PLING DATE: 1995-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH:: 6
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Pred. No. 4.2e+02;
2; Mismatches 0; Indels
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90.0%; Score 27; DB 10;
Best Local Similarity 83.3%; Pred. No. 6.7e+05;
Matches 5; Conservative 1; Mismatches 0
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US-09-919-703-3
                                                                                                                                                                                    Sequence 6887, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Caenorhabditis elegans US-10-369-493-6887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.3%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                              170 SVDIEY 175
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                    1 SVDVEY 6
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERRORS: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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Sequence 25, Application US/09862027

Sequence 25, Application US/09862027

Sequence 25, Application US/09862027

Sequence 25, Application US/09862027

TITLE COURTENT: Hodge, Martin R.

TITLE COF INVENTION: NO. US20020142428Alel Kinases and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 891
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                                                                                                                                                                                       100.0%; Score 30; DB 12; Length 414; 100.0%; Pred. No. 95;
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                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                         0; Mismatches
                                                                                          FEATURE:
, OTHER INFORMATION: Modified strep protein US-10-300-215-253
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Sequence 5723, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:
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                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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ORGANISM: Hydra vulgaris
US-09-862-027-25
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 1207
SEQ ID NO 253
LENGTH: 414
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Gaps
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Publication No. US20030008344A1
GENERAL INFORMATION:
APPLICANT: ADLER, JON ELLIOT
APPLICANT: ZOZULYA, SERGEY
APPLICANT: C'CONNELL, STADONG
APPLICANT: G'CONNELL, STADONG
APPLICANT: G'CONNELL, LENA
TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
FILE REFERENCE: 070803/0277470/RXT
CURRENT APPLICATION NUMBER: 60/187,546
PRIOR APPLICATION NUMBER: 60/187,546
PRIOR PILING DATE: 2000-03-07
PRIOR PLING DATE: 2000-03-07
PRIOR PLILNG DATE: 2000-04-07
PRIOR PPLICATION NUMBER: 60/195,536
PRIOR PLILNG DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/209,840
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Sequence 12, Application US/10193896

Publication No. US20030129710A1

GENERAL INFORMATION:
APPLICANT: Bioteknologiak Institut
APPLICANT: Bioteknologiak Institut
APPLICANT: Grognard, Peter
APPLICANT: Bethelsen, Flemming
APPLICANT: Brithauer, Kristian
APPLICANT: Eriknauer, Kristian
APPLICANT: Brithauer, Kristian
APPLICANT: Brithauer, Karen
APPLICANT: Brithauer
APPLICAN
                                                                                                                                Score 27; DB 12; Length 391;
Pred. No. 4.2e+02;
1; Mismatches 0; Indels
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TYPE: PRT ORGANISM: Gallid herpesvirus 3
                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                        347 SMDVEY 352
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451 AVDVEY 456
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US-10-193-896-12
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US-10-193-896-12
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US-09-799-629-14
                                                                US-10-209-967-14
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US-10-209-967-14

Sequence 14, Application US/10209967

Sequence 14, Deplication US/10209967

Bublication No. US20030171279A1

GENERAL INFORMATION:
TAPLICANT: MOIZMAN, BERNARD

TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS

TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS

CURRENT APPLICATION NUMBER: US/10/209,967

CURRENT PILING DATE: 2002-07-31

PRIOR APPLICATION NUMBER: 60/308,929

PRIOR FILING DATE: 2001-07-31

NUMBER: OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

LENGTH: 391
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                                                                                                                                                                                                                                                            APPLICANT: Haake, David A.

APPLICANT: Haake, David A.
Shang, Ellen S.
TITLE OF INVENTION: Leptospira MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/992,807
FILING DATE: 16-Jan-2002
CLASSIFICATION: «Unknown>
PRIOR APPLICATION: «Unknown>
PRIOR APPLICATION NUMBER: US/09/992,807
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WORM WASHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5656-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-992-807-6
                                                                                                                                                                ; Sequence 6, Application US/09992807; Patent No. US20020127240A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
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Best Local Similarity 83.3
Matches 5, Conservative
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23 TVDVEY 28
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1 TVDVEY 6
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US-09-992-807-6
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RESULT 19
US-10-190-417-25
Sequence 25. Application US/10190417
Publication No. US2003166137A1
GENERAL INFORMATION:
APPLICANT CARAT CARINE S.
APPLICANT Ryba, Nicholas J. P.
APPLICANT Chandrashekar, Jayaram
APPLICANT Chandrashekar, Jayaram
APPLICANT Chang, Yifeng
APPLICANT Chang, Yifeng
APPLICANT The Regents of the University of California
APPLICANT The Regents of the University of the
APPLICANT The Regents of the University of the
APPLICANT Begents of the University of the
APPLICANT THE GOVERNMENT OF THE SEcretary of the
APPLICANT BE REPRENCE 202130US
TILLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric Taste
TILLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric CURRENT FILING DATE: 201310US
CURRENT FILING DATE: 201310US
CURRENT FILING DATE: 2010-03-10
PRIOR APPLICATION NUMBER: US 60/3302,898
PRIOR APPLICATION NUMBER: US 60/3302,998
PRIOR FILING DATE: 2010-08-10
PRIOR FILING DATE: 2010-08-10
PRIOR FILING DATE: 2010-08-10
PRIOR FILING DATE: 2010-08-10
PRIOR FILING DATE: 202-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 25
LENGTH: 858
LENGTH: 858
LENGTH: 858
LENGTH: 858
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                                                                                                                                                                                                                                                                                                                             90.0%; Score 27; DB 12; Length 85
83.3%; Pred. No. 9.8e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 12; Length 85
Pred. No. 9.8e+02;
1; Mismatches 0; Indels
FILE REFERENCE: 36-002810US/PC
CURRENT APPLICATION NUMBER: US/10/246,785
CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: US 60/323,450
PRIOR PILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 858
TYPE: PAT
ORGANISM: Rattus norvegicus
US-10-246-785-9
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US-10-179-373-4
; Sequence 4, Application US/10179373
; Dublication No. US20030232407A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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US-10-190-417-25
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ryba, Nicholas J.P.
APPLICANT: Ryba, Nicholas J.P.
APPLICANT: Nelson, Greg
APPLICANT: Chandrashekar, Jayaram
APPLICANT: Chandrashekar, Jayaram
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Regents of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: as represented by the Secretary of the
APPLICANT: as represented by the Secretary of the
APPLICANT: Mammalian Sweet Taste Receptors
FILE REFERENCE: 023078-120110US
CURRENT FILING DATE: 2001-08-10
FRICH FILING DATE: 2001-09-03
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 25
LENGTH: 858
                                                                                                                                                                                                                                                                                                                                  90.0%; Score 27; DB 11; Length 858; 83.3%; Pred. No. 9.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 27; DB 11; Length 858; 83.3%; Pred. No. 9.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: rat T1R3 sweet taste receptor
US-09-927-315-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
US-10-246-785-9
Sequence 9, Application US/10246785
Subjication No. US2030148448A1
GENERAL INFORMATION:
APPLICANT: IRW, LLC
APPLICANT: The Scripps Research Institute
APPLICANT: The Scripps Research Sapplicant:
APPLICANT: Sheng, Ding
APPLICANT: Schultz, Peter G
TITLE OF INVENTION: Sweet Taste Receptors
          PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: 60/226,448

PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: 60/259,227

PRIOR PILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 14

LENGTH: 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 17
US-09-927-315-25
US-09-927-315-25
Sequence 25, Application US/09927315
Publication No. US20030040045A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Rattus sp.
                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-799-629-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 12; Length 18;
Pred. No. 26;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | | |
568 AVDVEY 573
                                                                                                      456 SVDMEY 461
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                                           1 SVDVEY 6
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APPLICANT: II, XIAODONG
APPLICANT: STASZEMSKI, LENA
APPLICANT: O'CONNELL, SHAMN
APPLICANT: O'CONNELL, SHAMN
APPLICANT: O'CONNELL, SHAMN
APPLICANT: ZOZULYA, SERGEY
APPLICANT: ADLER, JON
APPLICANT: ADLER, JON
APPLICANT: XU, HONG
APPLICANT: XU, HONG
APPLICANT: TILE FERNANDO
ITILE OF INVENTION: TIR HTERRO-CLICOMERIC TASTE RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
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ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THERBOF FOR
ITILE OF INVENTION NUMBER: 60/304,749
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-01-21
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2002-04-15
PRIOR FILING DATE: 2002-04-15
PRIOR FILING DATE: 2002-04-15
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 19
INVENTIOR OF SEQ ID NOS: 19
INVENTIOR DATE: 2002-04-22
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US-10-035-045-14

| Sequence 14, Application US/10035045
| Publication No. US20030054448A1
| GENERAL INFORMATION:
| APPLICANT: ADLER, JON BLIOT
| APPLICANT: LI, XIAODONG
| APPLICANT: C) CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: DO'CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: DO'CON-0280681
| FILE REFERENCE: 078003-0280681
| FILE REFERENCE: 078003-0280681
| CURRENT FILING DATE: 2002-01-03
| PRIOR APPLICATION NUMBER: 60/259,27
| PRIOR APPLICATION NUMBER: 60/259,27
| PRIOR PILING DATE: 2001-04-19
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NO 14
| LENGTH: 858
| LENGTH: 858
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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RESULT 23

US-10-193-477-56

J Sequence 56, Application US/10193477

Publication No. US20030195163A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: THEREOF

TITLE OF INVE
US-10-369-493-1385

// Sequence 1285, Application US/10369493

// Sequence 1285, Application US/10369493

// Sequence 1285, Application No. US20030233675A1

// GENERAL INPORMATION:
// APPLICANT: Hinkle, Green V.
// APPLICANT: Gldman, Barry S.
// APPLICANT: Goldman, Barry S.
// APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Gaps
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APPLICANT: Spaderal A.
APPLICANT: Spaderal A.
APPLICANT: Shinkete, Richard A.
APPLICANT: Shinkete, Richard A.
APPLICANT: Shinkete, Richard A.
APPLICANT: Muralidhara, Padigaru
APPLICANT: Spice, Sinberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-620 C1P
CURRENT APPLICATION NUMBER: US/09/737,149
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR PELING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR PAPLICATION NUMBER: 60/173,362
PRIOR PELING DATE: 1999-12-27
PRIOR PELING DATE: 1999-12-29
PRIOR FILING DATE: 2000-01-04
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE
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66.7%; Pred. No. Se+02;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Pred. No. 5e+02;
2; Mismatches
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 60/174,962
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/223,929
; PRIOR PILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 49
; SOFTMARE: PATENTIN Ver. 2.0
; SEQ ID NO 42
; LENGTH: 284
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/09737149; Patent No. US20020077466A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%;
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Rattus norvegicus
US-09-737-149-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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2 AVDIEY 7
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                                                                                                                                                                                    APPLICANT: Spaderna, Steven A
APPLICANT: Spaderna, Steven A
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spytek, Kimberly A.
ITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: 1999-10-14
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR PLING DATE: 1999-12-27
PRIOR PLING DATE: 2000-01-07
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US-09-737-149-42

US-09-737-149-42

US-09-737-149-42

Squence 42, Application US/09737149

Patent No. US20020077466A1

GENERAL INFORMATION:

APPLICANT: Spadern K

APPLICANT: Shimkers, Richard A.

APPLICANT: Spinkers, Richard A.

APPLICANT: Muralidhara, Padigaru

APPLICANT: Muralidhara, Padigaru

APPLICANT: Spikek, Kimberly A.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

FILE REFERENT Spikek, Sinchard A.

FILE REFERENT Spikek, Sinchard A.

PRIOR PLICATION NUMBER: US/09/737,149

PRIOR APPLICATION NUMBER: 60/170,564

PRIOR APPLICATION NUMBER: 60/170,564

PRIOR APPLICATION NUMBER: 60/173,362

PRIOR PLILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: 60/173,544

PRIOR PLILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: 60/173,544

PRIOR PLILING DATE: 1999-12-29

PRIOR PLILING DATE: 1999-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT

LOCATION: (1)...(282)

LOCATION: (1)...(282)

OTHER INFORMATION: Where X is a residue at which the query and confer INFORMATION: subject seugnces are not identical.

US-09-737-149-43
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66.7%; Pred. No. 5e+02;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Consensus Sequence
    US-09-737-149-43
Sequence 43, Application US/09737149
Patent No. USZ0020017466A1
GENERAL INFORMATION:
APPLICANT: Spaderna, Steven K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Sequence 1049, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICATION: Chiamydia pneumoniae genomic sequence and polypeptides, fragment
ITILE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
ITILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1049
LENGTH: 358
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0
                                                                                                                                                                                                                                                 Length 322;
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                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                               86.7%; Score 26; DB 12; I
100.0%; Pred. No. 5.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 15;
Pred. No. 6.2e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US20030119018A1
| Publication No. US20030119018A1
| GENERAL INFORMATION:
| APPLICANT: OMURA, SATOSHI
| APPLICANT: ISHIKAWA, JUN
| APPLICANT: ISHIKAWA, JUN
| APPLICANT: SHIBA, TADAYOSHI
| APPLICANT: SHIBA, TADAYOSHI
| APPLICANT: HATTOR! MASAHIRA
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| FILE REFERENCE: 249-26
| CURRENT APPLICATION NUMBER: US/10/156,761
| CURRENT PILLING DATE: 2001-05-39
| PRIOR FILING DATE: 2001-06-02
| PRIOR FILING DATE: 2001-06-05
| NUMBER: OF SEQ ID NOS: 15109
| SEQ ID NOS: 15109
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19042
LENGTH: 322
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ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                          TYPE: PRT
CRGANISM: Anabaena PCC7120
US-10-369-493-19042
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-156-761-12808
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US-10-289-762-1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES
FILE REPERENCE: 38-10(5.052) B
CURRENT PELLING NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR SEQ ID NOS: 47374
SEQ ID NO 22955
LENGTH: 305
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US-10-369-493-19042
US-10-369-493-19042
Squence 19042, Application US/10369493
Fublication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Stater, Steven C.
APPLICANT: Cheman, Barry S.
APPLICANT: Chem, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
    APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT PILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16538
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                         86.7%; Score 26; DB 12; Length 287; 100.0%; Pred. No. 5.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22955, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Aeropyrum pernix
US-10-369-493-22955
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US-10-369-493-22955
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Sequence 2914, Application US/10369493
; Sequence 2914, Application US/10369493
; Publication No. US20030233675A1
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Gladman, Barry S.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: US (2020)
; FILE REFERENCE: 38-10 (52052)B
; FILE REFERENCE: 2003-02-28
; PRIOR APPLICATION UNMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; RIOR FILING DATE: 2002-02-28
; RIOR FILING DATE: 2002-02-28
; RIOR FILING DATE: 2003-02-28
; RIOR FILING DATE: 2003-02-28
; RIOR FILING DATE: 2003-02-28
; RIOR FILING DATE: 2003-03-49
; RIOR FILING DATE: 2003-03-49
; SEQ ID NOS: 47374
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Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                          Sequence 5999, Application US/09738626
; Publication No. US2020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: TATEISHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: TEREISHI, NACKO
APPLICANT: TEREISHI, NACKO
APPLICANT: SENOH, AKIHRO
APPLICANT: SENOH, AKIHRO
APPLICANT: SENOH, AKIHRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PELICATION NUMBER: UP 90/159162
PRIOR PELICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PARCENTIN VET: 3.0
SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 TVDIEY 271
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Best Local Similarity
Matches 4; Conserv
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54 VDVBY 58
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Galdman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: WIMPER: US/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13345
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1147, Application US/10369493

publication No. US20030233675A1

publication No. US20030233675A1

publication No. US20030233675A1

publication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Sarry S.

APPLICANT: Goldman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 395;
                                                                      86.7%; Score 26; DB 12; Length 358; 100.0%; Pred. No. 6.4e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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86.7%; Score 26; DB 12; L

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT CRGANISM: Aspergillus nidulans US-10-369-493-13245
                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5; Conservative
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148 VDVEY 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VDVEY 6
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US-10-369-493-13245
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
US-10-369-493-1147
              US-10-289-762-1049
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Gaps

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Sequence 21, Application US/10093037
Sequence 21, Application US/10093037
Sequence 21, Application US/20030078397A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICAN
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APPLICATION WYBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A
REGISTRATION NUMBER: 38,347
TELECOMONICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 21:
SEQUENCYH: 511 anino acids
TYRE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.7%; Score 26; DB 14; I
100.0%; Pred. No. 9.4e+02;
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PRIOR FILING DATE: 2001-07-20
PRIOR PELING DATE: 1090-08-13
PRIOR PELING DATE: 1996-08-13
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Thermococcus chitonophagus US-10-093-037-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10461747
Publication No. US20030232378A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                Sequence 11, Application US/10193896

Sequence 11, Application US/10193896

Publication No. US20030129710A1

GENERAL INFORMATION:

APPLICANT: Bioteknologisk Institut

APPLICANT: Jorgensen, Flemming

APPLICANT: Brotesen, Flemming

APPLICANT: Stougaard, Peter

APPLICANT: Brithaner, Kristian

APPLICANT: Brithaner, Britha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%; Score 26; DB 16; Length 496; 66.7%; Pred. No. 9.1e+02; ive 2; Mismatches 0; Indels
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Publication No. US2002015555041

GENERAL INFORMATION:

TITLE OF INVENTION: GLYCOSIDASE ENZYMES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSE: Gray Cary Ware & Freidenrich LLP

STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego
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ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Window95
SOFTWARE: FastESQ for Window9 Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/10/121,032
FILING DATE: 09-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-199
APPLICATION NUMBER: 08/949,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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451 AIDVEY 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: T.maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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US-10-121-032-21
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TYPE: PRT
ORGANISM: Unknown Organism
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Pred. No. 1e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tarminoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANTON NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,308
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PRILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE FastsEQ for Windows Version 4.0
SEQ ID NO 13170
HILL OF INVENTION: MOVEL TOLL MOLECULES AND USES THEREOF
FILE REFERENCE: MNI-085
CURRENT APPLICATION NUMBER: US/10/461,747
CURRENT APPLICATION NUMBER: US/10/461,747
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/586,340
PRIOR FILING DATE: 1000-06-02
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PALENTIN VOR: 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 572;
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66.7%; Pred. No. 1.1e+03;
ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13170, Application US/09815242
Parent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13170
                                                                                                                                                                                                                                                                                                                                                                                                86.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
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CRGANISM: Homo sapiens
US-10-461-747-2
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518 SIDLEY 523
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Best Local Similarity
Matches 4; Conserv
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ORGANISM:
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Sequence 18 Application (18/0954412)

Sequence 18 Application (18/0954412)

GENERAL NICORATION (1870)

APPLICANT SPITEK, KRIBERLY ANN

APPLICANT SPITEK, KRIBERLY ANN

APPLICANT SCORES AND SEQUENCE CORNERS TO APPLICANT STATE AND SEQUENCE TO APPLICANT SCORES AND SCORES AND SCORES APPLICANT SCORES AND SCORES AND SCORES APPLICANT SCORES AND SC
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Length 606;

DB 12;

86.7%; Score 26;

Query Match

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APPLICANT: MISHRA, VIENUS S.
APPLICANT: SPTEK, KINEBLY ANN
APPLICANT: SPTEK, KINEBLY ANN
APPLICANT: TAUPLES, RAYMOND J.
APPLICANT: TAUPLES, RAYMOND J.
APPLICANT: TAUPLES, RAYMOND J.
APPLICANT: OGNAM, LINE A.
APPLICANT: TOGRAM, LINE A.
APPLICANT: TOGRAM, STEVEN D.
APPLICANT: TOGRAM, STEVEN D.
APPLICANT: GORAM, LINE A.
APPLICANT: GORAM, LINE A.
APPLICANT: GREAGE, WAITE M.
APPLICANT: GREAGE, WAITE M.
APPLICANT: GREAGE, WAITE M.
APPLICANT: GREAGE, WAITE M.
APPLICANT: SHOWS, CHERRE A.
APPLICANT: STOWE, DAVID
APPLICANT: STOWE, DAVID
APPLICANT: GUNTHER, EXIX
APPLICANT: GUNTHER, EXIX
APPLICANT: GUNTHER, EXIX
APPLICANT: GUNTHER, SELVA
APPLICANT
APPLICAN
; ORGANISM: Unknown Organism
FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide
US-09-954-342-20
                                                                                                                                                       Length 606;
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                 RESULT 43
US-09-954-342-42
US-09-954-342-42

, Sequence 42, Application US/09954342

; Publication No. US20030170838A1

; GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conservat
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576 SIDLEY 581
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TITLE OF INVENTION: NOVEL POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THEREBY
FILES OF INVENTION: NOVEL POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THEREBY
FILES APPLICATION NUMBER: 06/917
PRIOR PAPLICATION NUMBER: 06/20,284
PRIOR APPLICATION NUMBER: 06/20,284
PRIOR PLILNG DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 06/20,284
PRIOR PLILNG DATE: 2001-01-10
PRIOR PLILNG DATE: 2001-01-11
PRIOR PLILNG DATE: 2001-01-11
PRIOR PLILNG DATE: 2001-01-11
PRIOR PLILNG DATE: 2001-01-12
PRIOR PLILNG DATE: 2001-01-13
PRIOR PLILNG DATE: 2001-01-13
PRIOR PLILNG DATE: 2001-01-13
PRIOR PLILNG DATE: 2000-09-19
PRIOR PLILNG DATE: 2000-09-15
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                                      Gaps
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      Best Local Similarity 66.7%; Pred. No. 1.1e+03; Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTEK, KIMBELLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: COLMAN, LINDA
APPLICANT: TCHERNEY, VELIZAR T.
APPLICANT: SHENOY, SURESH
APPLICANT: GERLACH, WIRALIDHARA
APPLICANT: GERLACH, VALERIE L.
APPLICANT: GERLACH, VALERIE L.
APPLICANT: SMITHSON, GLENNDA
APPLICANT: SMITHSON, GLENNDA
APPLICANT: STONE, DAVID
APPLICANT: STONE, DAVID
APPLICANT: STONE, DAVID
APPLICANT: ELLERWAN, KAREN
APPLICANT: ELLERWAN, KAREN
                                                                                                                                                                                                                                                        RESULT 42
US-09-954-342-20
'Sequence 20, Application US/09954342
', Publication No. US20030170838A1
', GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LI, LI
RASTELLI, LUCA
ZERHUSEN, BRYAN
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576 SIDLEY 581
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APPLICANT: Ulauly, account a particle of the word;
APPLICANT: Tiehkoff, Daniel
APPLICANT: Tiehkoff, Daniel
APPLICANT: Tiehkoff, Daniel
APPLICANT: Zerobkin, Alexey M
APPLICANT: Ercebkin, Alexey M
APPLICANT: Lemieux, Sebastien M
ITLE OF INVENTION: Methods of Use
ITLE OF INVENTION: Methods of Use
FILE APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3395
LENGTH: 694
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100.0%; Pred. No. 1.3e+03;
Live 0; Mismatches 0;
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT PEDILOCATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALENTIN VOVEE: JP
SOFTWARE: PALENTIN VEY: 2.1
SOFTWARE: PALENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3395, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 47
20-10-128-714-8395
; Sequence 8395, Application US/10128714
; Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3395
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-749-2513
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576 SIDLEY 581
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US-10-128-714-3395
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Sequence 4, Application US/10193477

Sequence 4, Application US/10193477

PUDIcation No. US2003019516311

GENERAL INFORMATION:

TITLE OF INVENTION: ELICITED RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: D0153 NP

CURRENT APPLICATION NUMBER: US 60/304,888

PRIOR FILING DATE: 2002-07-11

PRIOR APPLICATION NUMBER: US 60/372,147

PRIOR APPLICATION NUMBER: US 60/372,147

WUMBER OF SEQ ID NOS: 229

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 606

THEORY FILING

LENGTH: 606

THEORY FILING

SEQ ID NOS: 229

SEQ ID NOS: 229
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                                                                                                                                                                                                                   Query Match 86.7%; Score 26; DB 12; Length 606; Best Local Similarity 66.7%; Pred. No. 1.1e+03; Matches 4; Conservative 2; Mismatches 0; Indels
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Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: SCGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: STO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISANO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: INGAI, KEIICHI
APPLICANT: IRE, RYOTARO
         PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
LENGTH: 606
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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Best Local Similarity 66.7
Matches 4; Conservative
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ORGANISM: Homo sapiens
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576 SIDLEY 581
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RESULT 49

US-10-369-493-22944

Sequence 22944, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Binkle, Gregory J.

APPLICANT: Goldman, Barry S.

APPLICANT: SAFORMATION: Colored S.

FILE REPERENCE: 30-10-2-8

PRIOR PRIOR DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR BARRY FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 22944

LENGTH: 784
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; Sequence 281, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT FAPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SEQ ID NO 281
; LENGTH: 968
; TENGTH: 968
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; ORGANISM: Aeropyrum pernix
US-10-369-493-22944
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Best Local Similarity 83.3
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-10-291-265-281
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283 SVEVEY 288
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            214 VDVEY 218
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GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wend;
APPLICANT: Hu, Wend;
APPLICANT: Hu, Wend;
APPLICANT: Hu, Wend;
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REPERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
FILE REPERENCE: 2001-04-23
FRIOR PELLING DATE: 2001-04-23
FRIOR PELLING DATE: 2001-04-27
FRIOR PELLING DATE: 2001-04-27
FRIOR PELLING DATE: 2001-06-05
FRIOR PELLING DATE: 2001-06-05
FRIOR PELLING DATE: 2001-06-09
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2001-09-09
FRIOR FILING DATE: 2001-09-09
FRIOR FILING DATE: 2001-09-31
NUMBER OF SEQ ID NOS: 8603
SOFFWARE: Patentin version 3.1
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WEAULY 48

WEAULY 4911-017, Application US/10369493

Sequence 4017, Application US/10369493

Publication No. U320030233675A1

SEQUENCE 4017, Application US/10369493

SEQUENCE 4017, Application US/10369493

APPLICANT: Cao, Yongwei

APPLICANT: Stater, Steven C.

APPLICANT: Stater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 4017

LENGTH: 225
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86.7%; Score 26; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels
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: LOCATION: (1)..(725)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-4017
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-8395
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Best Local Similarity 100.
Matches 5; Conservative
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Search completed: January 20, 2004, 14:02:42

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Sequence 18, Appl
Sequence 3, Appl
Sequence 3, Appli
Sequence 4507, Ap
Sequence 4507, Ap
Sequence 7104, Ap
Sequence 31787, A
Sequence 32787, A
Sequence 471, Appli
Sequence 471, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 1049, Ap
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US-08-759-59-1
US-08-759-59-1
Sequence 1, Application US/08759599
Sequence 1, Application US/08759599
Sequence 1, Application US/08759599
Sequence 1, Application US/08759599
SEREAL INFORMATION:
APPLICANT: Rabkin, Simon
APPLICANT: Rabkin, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 4088hington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ၀
US-07-854-596B-43

US-07-854-596B-47

US-07-854-596B-40

US-09-211-542A-4

US-08-488-940-3

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US-08-488-940-3

US-08-488-940-1

US-08-488-940-1

US-08-488-940-1

US-09-345-473E-25

US-09-345-473E-25

US-09-345-473E-25

US-09-345-473E-25

US-09-345-473E-25

US-09-345-473E-25

US-09-325-941-14

US-09-328-32A-5104

US-09-328-33A-5104

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
 Sequence 6, Applisequence 7, Applisequence 14, Applisequence 12, Applisequence 13, Applisequence 3, Applisequence 4, Applisequence 1, Applisequence 1, Applisequence 1, Applisequence 12, Applisequence 2, Applisequence 26, Applisequence 26, Applisequence 19, Applisequence 15, Applisequence 
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11.539 Million cell updates/sec
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Sequence 5,
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-294-457-1

US-09-294-457-1

US-08-759-599-6

US-08-759-599-6

US-08-759-599-6

US-09-294-457-7

US-09-294-457-7

US-09-211-542A-114

US-09-211-542A-114

US-09-374-038-3

US-09-658-179-4

US-09-658-179-4

US-09-658-179-1

US-09-658-179-2

US-09-658-179-2

US-09-658-179-2

US-09-658-179-2

US-09-658-179-2

US-09-658-179-2

US-09-658-179-2

US-09-658-179-2

US-09-658-158-158-19
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries
                                                                    protein search, using sw model
                                                                                            January 20, 2004, 13:54:52
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                          seg length: 0
seg length: 200000000
                                                                                                                                     US-09-919-703-1
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Match Length
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Perfect score:
                                                                                                                                                                                                 Scoring table:
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Maximum DB
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                                                                                            Run on:
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No.
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APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348567el Peptides and Their Use to TITLE OF INVENTION: No. 6348567el Peptides and Their Use to TITLE OF INVENTION: Ameliate Cell Death
FILE REPERENCE: 50216/03003
CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-41.9
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 4; Length 16; 100.0%; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0; Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,599
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
ATTONENY/AGENT INFORMATION:
NAME: MCMASTER; David D.
REGISCHATION NUMBER: 33,963
REGISCHATION NUMBER: 33,963
REFRENCE/DOCKET NUMBER: 780059.401
TELEFORM/UNICATION INFORMATION:
TELEFORM/UNICATION INFORMATION:
TELEFORM/UNICATION INFORMATION:
TELEFORM/UNICATION INFORMATION:
TELEFORM/UNICATION INFORMATION:
TELEFORM/UNICATION: (206) 682-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Synthetic polypeptide US-09-294-457-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
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Patent No. 5917013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 6; Conservative
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STRANDEDNESS: sir
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Patent No. 6348567

GENERAL INFORMATION:

APPLICANT: Krystal, Gerald

APPLICANT: Rabkin, Simon W.

TITLE OF INVENTION: Amelicate Cell Death

FILE REFERENCE: 50216/003003

CURRENT FILING DATE: 1999-04-19

FRIOR PAPLICATION NUMBER: US/09/294,457

CURRENT FILING DATE: 1999-04-19

PRIOR FILING DATE: 1995-12-05

PRIOR FILING DATE: 1995-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 6

LENGTH: 6
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                               CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,599

FILING DATE: 05-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MCMASters, David D.

REGISTRATION NUMBER: 780059.401

TELEPRATION NUMBER: 780059.401

TELEPRATION NUMBER: 2060

TELEPRATION: (206) 682-6031

TELEPRATION: (206) 682-6031

TELEPRATION: CROWNING TO THE COMMUNICATION TO THE COMMUNICATI
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Synthetic polypeptide
US-09-294-457-1
          PC-DOS/MS-DOS
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Sequence 5, Application US/09294457

Patent No. 6348567

GENERAL INPORMATION:

APPLICANT: Krystal, Gerald
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: peptide
US-08-759-599-1
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Best Local Similarity
Matches 6; Conserv
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US-09-294-457-1
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Query Match
Best Local Similarity
Matches 6; Conserve
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Matches
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Patent No. 6348567
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Patent No. 5917013
GENERAL INFORMATION:
                                                                                                                                   GENERAL INFORMATION:
               APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348567el Peptides
TITLE OF INVENTION: Ameliorate Cell Death
FILE REFERENCE: 50216/003003
CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,599
FILLING DATE: 05-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE
TITLE OF INVENTION: AMELIORATE CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (200, mer.ex; 3723836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington
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linear
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100.0%; Pred. No. 1.3;
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                 and Their Use
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                                                                               Matches
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; MOLECULE TYPE: peptide US-08-759-599-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-759-599-7
                                                                                                                                                                 TELEPAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 20
                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/759,599
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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Patent No. 591701
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APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washing
                                                                                                                                              TOPOLOGY:
                                                                                                                                                            STRANDEDNESS:
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1 SVDVEY 6
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Similarity 100.0%;
6; Conservative 0
                                           Similarity 6; Conserv
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                                                                                                                                           iss: single
linear
                                                         100.0%; Score 30; DB 2; 100.0%; Pred. No. 1.4;
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US-09-211-542A-14
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CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION: 1653
PRIOR APPLICATION NUMBER: 60/069,497
APPLICATION NUMBER: 60/069,497
APPLICATION TIPORMATION:
APPLICATION TOPORMATION:
APPLICATION TOPORMATION:
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LENGTH: 21
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Reed,
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TITLE OF INVENTION: No. 6348567el Peptides and Their Use
TITLE OF INVENTION: Ameliorate Cell Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Krystal, Gerald APPLICANT: Rabkin, Simon
TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                              NAME: Attorney, Strimpel, Harriet M. REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                               TELEPHONE:
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                                                               (617)443-9292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guy L.
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Pred. No.
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RESULT 11 US-07-854-596B-31

Patent No. 5434073 GENERAL INFORMATION:

l, Application US/07854596B 5434073

APPLICANT:

Dawson, Keith M Hunter, Michael G Czaplewski, Lloyd

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US-09-211-542A-12
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Best Local 9
                                                               Matches
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/211,542A

FILING DATE: 15-December-1998

CLASSIFICATION DATA:

APPLICATION UMBER: 60/069,497

FILING DATE: 15-December-1997

APPLICATION NUMBER: 60/069,497

FILING DATE: 15-December-1997

APPLICATION TORNEYS HORD: Harrier M
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Patent No. 6210667
                                                                                                                                                                                          TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                             NAME: Attorney Strimpel, Harriet M.
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, G
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TOPOLOGY:
                                                             Local Similarity hes 6; Conserv
                                                                                                                                                                        TYPE: amino acid
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Local Similarity 100.0%;
Local Similarity 100.0%;
les 6; Conservative 0
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99 SVDVEY 104
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                                                                              100.0%;
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                                                                                Score 30; DB
Pred. No. 31;
                                                               Mismatches
                                                                                            Length 356;
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TITLE OF INVENTION: PRINCES OF SEQUENCES: 7

Proteins and nucleic acids

ADDRESSEE:

Chicago

Ten South Wacker Drive, Suite 3000

Dr. John J. McDonnell

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                                                                                         ; LENGTH: 372
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-374-038-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-374-038-3
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                                 Matches
                                                           Query Match
                                                                                                                                                          SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                     Patent No. 6309873
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6309873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
TOPOLOGY: line

(OLECUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312,715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/854,596B

FILING DATE: 03-UN-1992

CHARCYTER 03-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-715-1234
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                             Similarity 6; Conserv
 SVDVEY 6
                                                                                                                                                                           PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                   Menendez, Alina Seralena
Escalona, Elder Pupo
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                            100.0%; Score 30; DB ilarity 100.0%; Pred. No. 33; Conservative 0; Mismatches
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ilarity 100.0%;
Conservative 0
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La Fuente
                                                           DB 4; Length 372;
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APPLICANT: Menendez, Alina Garcia
APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14
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Best Local Similarity
Wetches 6; Conserve
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APPLICANT: Griego, Martha De Jesus Gonzalez
FILE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14
Patent No. 6413759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-658-179-3
                                                                                                                                                                                             SEQ ID NO 4
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                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09374038 Patent No. 6309873
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/658,179
CURRENT FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                          LENGTH: 384
TYPE: PRT
ORGANISM: Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 372
TYPE: PRT
ORGANISM: Streptococcus equisimilis
                                                             Local Similarity
mes 6; Conserv
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157 SYDVEY 162
157 SVDVEY 162
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                               1 SYDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVDVEY 6
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Garcia, Jose De Jesus De
Ojalvo, Ariana Garcia
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Garcia, Jose De Jesus De
Ojalvo, Ariana Garcia
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Escalona, Elder Pupo
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                                                               Conservative
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                                                             100.0%; Score 30; DB
100.0%; Pred. No. 34;
tive 0; Mismatches
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                                                                                             DB 4; Length 384;
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RESULT 17
US-09-658-179-1
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SEQ ID NO 1
LENGTH: 401
TYPE: PRT
ORGANISM: Streptococcus equisimilis
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Matches
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PATENT NO. 6309873
CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
GENERAL INFORMATION: APPLICANT: Madrazo
                                   Sequence 1, Application US/09658179 Patent No. 6413759
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APPLICANT:
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LENGTH: 384
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Best Local Similarity
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APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Ojalvo, Ariana Garcia
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CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREEFFOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
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Garcia, Jose De Jesus De La Fuente
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Escalona, Elder Pupo
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Isis Del Carmen
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100.0%; Pred. No. 36;
tive 0; Mismatches
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APPLICANT: Garce,
APPLICANT: Ojalvo, Ariana Garce,
APPLICANT: Menendez, Alina Seralena
APPLICANT: Mesendez, Alina Seralena
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASS MUTANTS
TTTE PREPERENCE: Sequence Listings 1-14 re: 976-5
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US-08-759-599-12
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TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-179-1
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Best Local Similarity 100.0%; Pred. No.
Matches 6; Conservative 0; Mismatch
Query Match
Best Local Similarity
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APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
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CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                       TELEX: 3723836
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 780
                                                                                                                                                                                                                                                                                                            NAME: McMasters, David REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/759,599
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                               TELEFAX:
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   100.0%;
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   Score 30;
Pred. No.
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   DB 2;
37;
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                     Length 413;
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RESULT 20
US-09-294-457-12
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US-09-374-038-2
                                                                                                                                       US-09-294-457-12
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
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Best Local :
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SEQ ID NO 2
                                                             Matches
                                                                             Best Local Similarity
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Rabkin, Simon W.
APPLICANT: Rabkin, Simon W.
ITLE OF INVENTION: No. 6348567el Peptides and Their Use to
TITLE OF INVENTION: Ameliorate Cell Death
FILE REFERENCE: 50216/003003
CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR PILING DATE: 1996-12-05
PRIOR PILING DATE: 1995-12-06
PRIOR PILING DATE: 1995-12-06
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CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
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                                                                                                                                                       OTHER INFORMATION: Synthetic polypeptide
                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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   1 SVDVEY 6
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                                                           6; Conservative
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Garcia, Jose De Jesus De La Fuente
Ojalvo, Ariana Garcia
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Escalona, Elder Pupo
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                                                           100.0%; Score 30; DB 4; Length 413; 100.0%; Pred. No. 37; ive 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-179-2
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Patent No. 6210667
GENERAL INFORMATION:
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATENT NO. 6413759
CURRENT APPLICATION NUMBER: US/09/658,179
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
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APPLICANT: Garcia, Jose De Jesus De La Fuent
APPLICANT: Ojalvo, Ariana Garcia
APPLICANT: Menendez, Alina Seralena
APPLICANT: Escalona, Elder Pupo
APPLICANT: Hasso, Julio Raul Fernandez
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR POPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                     NAME: Attorney, Strimpel, Harriet M.
REGISTRATION NUMBER: 3,708
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: BAC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                 FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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CITY: Boston
STATE: Massac
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                                                         TELEPHONE:
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Garcia, Jose De Jesus De La Fuente
Ojalvo, Ariana Garcia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BROMBERG & SUNSTEIN, LLP
                                                         (617)443-9292
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RESULT 23
5240845-1
;Patent No. 5240845
; APPLICANT: FUJI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FUJII, SETSURO;TAKADA, KAORUKO;. KATANO, TAMIKI
MAJIMA, EIJI;OGINO, KOICHI;ONO, KENJI;SAKATA, YASUYO;UENOYAMA,
TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/07854596B Patent No. 5434073
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APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MUTATED STREPTOKINASE PROTEINS NUMBER OF SEQUENCES: 65 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/549,049
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   STREET: 1em -
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Local Similarity 100.0%;
hes 6; Conservative 0
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                                                                                                                                                                                                                                                            COUNTRY:
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                   92,337
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Pred. No. 37;
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Pred. No. 37;
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US-07-854-596B-19
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Best Local Similarity
Matches 6; Conserv
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                                                               Matches
                                                                              Query Match
Best Local |
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
                                                                                                                                                                                                                                                                        NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0:
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 415 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                            MOLECULE TYPE: protein
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ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 10.
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                                                                                                                                                                                                                                TELLEFAX: 510-221
                                                                                                                                                             LENGTH: 435 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
178 SVDVEY 183
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                               1 SVDVEY 6
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                                                              Similarity 6; Conserv
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                                                            100.0%; Score 30; DI
100.0%; Pred. No. 39;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                        92,337
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RESULT 26 US-07-854-596B-15

Sequence 15, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:

APPLICANT: APPLICANT:

PPLICANT: Dawson, Keith M
PPLICANT: Hunter, Michael G
PPLICANT: Hunter, Michael G
PPLICANT: Czaplewski, Lloyd G
ITLE OF INVENTION: Proteins and nucleic acids

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US-08-560-098A-52
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Matches
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TELEX: 910-221-3317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Proteins having Fibrinolytic and TITLE OF INVENTION: Coagulation-inhibiting Properties NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
PRIOR APPLICATION DATA
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                                                                                                                                                                                                      STREET: 1200
CITY: Washington
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Chicago
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REGISTRATION NUMBER: 26,949
REFERENCE/DOCKST NUMBER: 92,337
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les 6; Conserv
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TELEFAX: 312-715-1234
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1200 G Street, N.W., Suite 700
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ilarity 100.0%;
Conservative 0
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Pred. No. 40;
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100.0%;

Best Local Similarity 100.0%;

Matches 6; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                    TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: P 44 40 8
FILING DATE: 17-MOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                            TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Czaplewski, Lloyd
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 440 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 100.0%; Score 30; Similarity 100.0%; Pred. No. 6; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60606
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                                                                                                                                                        483 amino acids
                                                                                                                                                                                                                               312-715-1234
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                                                                                                    protein
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                               Score 30; DB
Pred. No. 44;
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                                               DB 1; Length 483;
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Mismatches

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Gaps

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226 SVDVEY 231

SYDVEY

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RESULT 30
US-07-854-596B-28
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US-07-854-596B-47
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                           Sequence 28, Application US/07854596B Patent No. 5434073
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47, Application US/07854596B Patent No. 5434073
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
                                                                                                                      TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 10.
                                                                                                   ORRESPONDENCE ADDRESS:
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tes 6; Conservative
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715-1234
771 5217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: IL
COUNTRY: USA
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COUNTRY: U
                                                                                   ADDRESSEE:
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                                               Chicago
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     ASĎ
                                                                 E: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 amino acids
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 31
US-09-211-542A-4
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,54
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                          TELEFAX: (617)443-000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
SEQUENCE CHARACTERISTICS:
LENGTH: 736 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BACTERIAL FIBRIN-I
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMBERG & SUNSTEIN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                  NAME: Attorney, Strimpel, H
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 18
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TOPOLOGY: linear
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REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 499 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 Summer Street
                                                                            (617)443-0004
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                                                                                                  (617)443-9292
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                                                                                                                                                                                                                                                                                                                 US/09/211,542A
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TOPOLOGY: linear

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Query Match
Best Local Similarity
"arches 6; Conserva
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US-09-211-542A-2
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US-07-854-596B-40
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                                                                                                                                                                                                                                                                                                                                            US-07-854-596B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UTW-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                 Sequence 2, Application US/09211542A Patent No. 6210667
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Matches 6; Conservative
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                                               GENERAL INFORMATION:
APPLICANT: Reed, C
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                      143 SVDVEY 148
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Ten South Wacker Drive,
                                                                                                                                                                                                                                                                                                                                                                                                              747 amino acids
                                                                                                                                                                                                                                                                         Conservative
BROMBERG & SUNSTEIN, LLP
                                                                   Guy L
                                                                                                                                                                                                                                                                                         100.0%;
                                               BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/211, FILING DATE: 15-December-1998 CLASSIFICATION: 1653 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/069,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Attorney, Strimpel, Harriet M. REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Har
                              TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                            NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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CITY: E
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                                                                 05433/009001
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Pred. No. 76;
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                                                                                                                                                                                                     Version #1.30
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US-07-854-596B-35

Sequence 35, Application US/07854596B

Patent No. 5434073

GENERAL INFORMATION:
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                                                                RESULT 36
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US-08-488-940-3
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                                                                                                                                                                                Matches
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APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/488,940
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                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 800 amino acids
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ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            TELLEFAX: 61
TELEFAX: 200154
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                                                                                                                                                                               Local Similarity
mes 6; Conserv
                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not
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Local Similarity 100.0%;
les 6; Conservative C
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                                                                                                                156 SVDVEY 161
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Pred. No. 78;
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Pred. No. 77;
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Query Match
Best Local Similarity
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US-09-345-473E-25
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US-09-345-473E-25
                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 891
                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hodge, Martin
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases of
TITLE OF INVENTION: No. 6558903el Kinases of
TITLE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILLING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09345473E
Patent No. 6558903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: MCDORNELL, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMMUNICATION INFORMATION:
TELEPIONE: 312-715-1000
TELEPIA: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 859 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INTENTION: Proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 03-JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 SVDVEY 183
1 SYDVEY 6
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illarity 100.0%;
Conservative 0
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                                  Score 30; DB
Pred. No. 87;
0; Mismatches
                                                                         DB 4; Length 891;
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137 SVDVEY 142

US-08-488-940-2

Sequence 2, Application Patent No. 5854049
GENERAL INFORMATION:

Application US/08488940

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US-08-488-940-2
                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08488940
Patent No. 5854049
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                      -08-488-940-1
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
ZIP: 02110-200.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/488,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                ADULTSTREET: STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 220.
CITY: Boston
                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
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eTREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                            E OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 SVDVEY 529
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                                                                                                                                                                                                                                                                            Guy L.
DN: PLASMIN-RESISTANT STREPTOKINASE
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Pred. No. 1.2e+02;
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Query Match
Best Local Similarity
"hes 6; Conserv:
                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-488-940-17
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Patent No. 5854049
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Best Local (
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                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTAN NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/00
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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STREET: 2-
STRY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLEFAX: 0.
TELEFAX: 200154
                                                                                                                         TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                         LENGTH:
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                                                                                                                                                         1194 amino acids
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                Conservative
                                                                                                                       not relevant
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                             100.0%; Score 30; DB 2;
100.0%; Pred. No. 1.2e+02;
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Pred. No.
                Mismatches
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                                            Length 1194;
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RESULT 41
US-08-488-940-18
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                                       SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 280
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                    Sequence 14, Application US/09470512A Patent No. 6376652
                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local (
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ADDLICANT: Reed, Guy
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/470,512A
CURRENT FILING DATE: 1999-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 18:
                                                                                     NUMBER OF SEQ ID NOS: 16
ORGANISM: Bacillus subtilis 9-470-512A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 01.54
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/488,940
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                                                                                                 1999-12-12
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                                                                                                                                US-09-294-457-3
                                                                                                ; Sequence 3, Application US/09294457; Patent No. 6348567
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GENERAL

INFORMATION:

APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348567el Peptides
TITLE OF INVENTION: Ameliorate Cell Death
FILE REFERENCE: 50216/003003
CURRENT PEPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19

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US-08-759-599-3
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Patent No. 5917
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Best Local Similarity
                                                   Matches
                                                               Query Match
Best Local
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TELEX: 3723836
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/759,599
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                     LENGTH:
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                                                l Similarity
5; Conserv
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1 TVDVEY 6
                       1 SYDVEY 6
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: Washington
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amino acid
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                                                   Conservative
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linear
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                                                                                                                peptide
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                                                               90.0%;
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Pred. No. 68;
                                                               Score 27; [
Pred. No. 2.
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
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RESULT 46
US-09-328-352-4507
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                                                                                                                                                                                                                                   TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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                                                                                                                                   Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/444,646
FILING DATE: 19-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5656-107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haake, David A.
APPLICANT: Shang, Ellen S.
TITLE OF INVENTION: Leptospira MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                 Local Similarity es 5; Conserv
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                                                              TVDVEY 28
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                                                                                                                                                   90.0%;
83.3%;
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Pred. No. 2.5e+05;
                                                                                                                                                   Score 27; DB 2;
Pred. No. 1.5e+02;
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RESULT 48
US-09-107-532A-5104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7836, Application US/09328352

Patent N. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUKANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7836
LENGTH: 626
LENGTH: 626
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: GARY L. BY AND AND AND AND ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4507
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                      Sequence 5104, Application US/09107532A Patent No. 6583275
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A DOUCETTE ACID
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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    COUNTRAL COUNTRAL COUNTRAL COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COUNTRER: PC
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 SVDVDY 235
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                                                                                                                                      STATE: Massachusetts
                                                                                                                                                             CITY: Waltham
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 2.8e+02;
Pred. No. 2.8e+02;
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Pred. No. 1.
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                                                                                                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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1.7e+02;
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Query Match
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US-08-713-885-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Applic
Patent No. 5985833
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,885
FILING DATE:
CLASSIFICATION: 514
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                      NFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5104:
                                                     REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mosesson, Mic
APPLICANT: Meh, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: THROMBIN INHIBITOR NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECHONE: (781)893-8077
TELECHONE: (781)893-8077
TELECHONE: (781)893-8077
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 53202-4497
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...885
SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVDVEY 6
X: (414) 271-3552
N FOR SEQ ID NO: 3:
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               Wisconsin
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/107,532A
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Pred. No. 4.1e+02;
1; Mismatches 0
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Search completed: January 20, 2004, 13:58:13
Job time : 23 secs

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US-09-134-001C-4271
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                                                                                                                             ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4271
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                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4271
LENGTH: 71
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Best Local Similarity
Matches 5; Conserv
                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4271, Application US/09134001C
                                                                                                                                                                                                                                                                                          APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE; GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
36
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                                1 SYDVEY 6
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SVDIDY 41
                                                                Conservative
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100.0%;
                                                                              86.7%;
                                                             Score 26; DB 'Pred. No. 42; 2; Mismatches
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Pred. No. 5.9;
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